

IN	WO200119868-A1.
X	22-MAR-2001.
X	D
X	15-SEP-1999; 99W0-KR00554.
X	(MOSA-) MOGAM BIOTECHNOLOGY RES INST.
X	A
X	I Chang J, Kim JS, Park EJ, Yum J, Chung S;
X	I
X	R WPI: 2001-244787/25.
X	R N-PDBB; ADD3255.
X	X Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated diseases, e.g. cancer and rheumatoid arthritis, has human apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid sequence
X	S Claim 4; Page 42-44; 50pp; English.
X	X The present sequence is human angiogenesis inhibitor, LK68 protein. LK68 protein contains the amino acid sequences of human apolipoprotein(a) kringle domains IV36 (LK6 Protein), IV37 (LK7 protein) and V38 (LK8 protein). LK68, LK6, LK7 and LK8 are inhibitors of endothelial cell proliferation, cell migration and normal development of capillaries in the chick embryo chorionicallantoic membrane (CAM). LK68 protein, its single chain equivalents or their functional equivalents, are useful for treating angiogenesis-mediated diseases, such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic disease in animals or humans. LK68 is useful as an anticancer agent and also for inhibiting primary tumour growth.
X	Sequence 308 AA;
X	Query Match Score 1786; DB 22; Length 308;
X	Best Local Similarity 100.0%; Freq. No. 1.e-107;
X	Matches 308; Conservatory 0; Mismatches 0; Indels 0; Gaps 0;
X	1 KSPVVQCYHDGDSYRGISSTTVGRTCSWSSMIPHWHORTPNYPNAGLTENYCRNP 60
X	1 KSPVVQDCYHDGDSYRGISSTTVGRTCSWSSMIPHWHORTPNYPNAGLTENYCRNP 60
X	61 DSGKOPWCYTDTPCVRYWCNITQSETESGVLETPPTVVPVPSMAHSAAPTEOTPVVR 120
X	61 DSQKQPWCYTDTPCVRYWCNITQSETESGVLETPPTVVPVPSMAHSAAPTEQTFAVR 120
X	121 QCYHGNQSRTGFSSTTIGRCQSSSMTHPHQRTPEVNAPPTVQVPSLGPSEODCMFNGKTYGRKKAT 180
X	121 QCYHGNQSRTGFSSTTIGRCQSSSMTHPHQRTPEVNAPPTVQVPSLGPSEODCMFNGKTYGRKKAT 180
X	181 WCFTTDPSIWIWEXCNLTCSDPSEGTVAPPTVQVPSLGPSEODCMFNGKTYGRKKAT 240
X	181 WCFTTDPSIWIWEXCNLTCSDPSEGTVAPPTVQVPSLGPSEODCMFNGKTYGRKKAT 240
X	241 TYTGTPCQEWAQEPHRISTFPGTKWAGLEYKNICRNPDGDINGPWCYTMMERKLFDYC 300
X	241 TYTGTPCQEWAQEPHRISTFPGTKWAGLEYKNICRNPDGDINGPWCYTMMERKLFDYC 300
X	301 DIPLCASS 308
X	301 DIPLCASS 308
SULT 2	B01918
AAB01918 standard; Protein; 189 AA.	18-SEP-2000 (first entry)

Use of angiotatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy

Claim 4; Page 128; 203pp; English.

The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiotatin fragment, a combination of angiotatin fragments, or aggregate angiotatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4BKLS protein. The aggregate angiotatin has a Mol. Wt of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy. The present sequence, bovine kringle 1-3, is a specific angiotatin fragment which can be used in the invention, and represents amino acids 6-255 of bovine angiotatin.

Sequence	250 AA;	Query Match	40.1%	Score	716;	DB	17;	Length	250;
		Best Local Similarity	42.1%	Prod.	NO.	8.6e-39;			
		Matches 12;	Conservative	Mismatches	43;				
					80;	Indels	50;	Gaps	7;

		Sequence	AA:
2	CTKIGNEOTVYGGTAAKSSTVTCWSTSPSPHPKKEPEKPKPLAGILENTCRNPNDENG	SO	
3	: : : : : : : : : : :	XX	
4	: : : : : : : : : : :	SO	
5	: : : : : : : : : : :	Sequence	250 AA:

Query	Match	Score	DB	Length
WCYTTDPVCYRIVWCYCNLIQCSSESGLIPTVYVPVMEAHSEAAPECTPVYRCYHGN	126	40.0%	715;	250;

UNIFORMING LITERACY IN A COUNTRY OF DIVERSE LANGUAGES

187	P.S.I.R.M.Y.C.A.L.R.U.S.T.D.G.T.V.A.P.P.V.I.Q.P.S.L.O.G.P.P.S.H.O.D.C.H.F.G.N.G.R.K.A.T.V.G.T.P	246	
			Q.Y

148 PQKRWEFCIDPRCT-----PSSGP-----KIQCLKGIGKNGGTAVITISGHT 193
149 PQQKQWEEFCIDPRCT-----PSSGP-----KIQCLKGIGKNGGTAVITISGHT 193
Db 61 WCYTIDPETERFDYDIDIPCED----EMHCS 87

QY 127 GQSYXGTSTTIVGRTTCOSWSSMTPHRQHTPENPVNDGLTMNYCIRPDADTGPNQFTTD 186
305 QY 127 GQSYXGTSTTIVGRTTCOSWSSMTPHRQHTPENPVNDGLTMNYCIRPDADTGPNQFTTD 186

194 CQRWSEQTPIKHNR-TPENFPCPKNLEENYCRNPDGS-KAPWCYTINSEWRWECTPSC 250
195 GEHYBKRISTKTMSSIECWSQGSPSHANGYLPSKPBPNKALKMAYCRNFDGEPRPWFTTD 147

Ov 187 PSIRMEYCNLTRCSDTGTVVAPPYILOVPSLGPSEODCMFGNGKSYRGKATTVGTP 246

AFN07369 standard; protein; 250 AA.

QY 24 / CQEWAKEPIKES FIPSINKAGLENTCPNDODINPCWJLMPAKLICDULPC
AMW07569;

22-JUN-1987 (first entrv) Dd 194 CQRWSAQSPHKIRN-TPENFCKNLLEENYCRNPDE-TAPWCYTIDSEVRYDCKTPSC 250

RESOLVED, That the Board of Directors of the American Academy of Orthopaedic Surgeons, at its meeting in New Orleans, Louisiana, November 19, 1949, accept the invitation of the International Society of Orthopaedics, Traumatology and Rehabilitation to participate in the Second International Congress of Orthopaedics, Traumatology and Rehabilitation, to be held in Paris, France, June 19-24, 1950.

AY02109; AC AC

16-JUL-1999 (first entry)
AA DT

WO963574-A2. XX Df A multifunctional protein of the invention

14-NOV-1996. D XX

26-APR-1996:	96NO-US05856,
	KW
	Argylosulfan
	Interferon-inducible protein
	Platelet factor 4
	Antiangiogenic

08-MAR-1996: 960US-0612788
 R anti-tumor; multivalent functional protein; angiogenesis-mediated disease;
 cancer; diagnosis; immunotherapy; mannan degradation antigen arachis.
 KW KW KW KW

b 166 WCFITDPNKRKELCDIPRCT-----TPP----PSSSGPTIQ--CLKGIGENVRGVAV 211
 Y 241 TVGTPQEQAAQSPHRESTEFGTINKWAGLEKNCRNPODINGPWCCTMANKPLKEDYC 300
 b 212 TVEGHTCQHNSAQTPTHINR-TPENFPCKNLDENYCRNPDSK-RAPWCHTNTSQRWEYC 269
 Y 301 DPLCLASS 308
 X ||| | | | |
 b 270 KTPSCDSS 277
 ESUET 10
 AG79748 Human plasminogen kringle domains 1-3, K1-3.
 D AAG79748 standard; Protein; 260 AA.
 X C AAG79748;
 X T 18-MAR-2003 (first entry)
 X E Human plasminogen kringle domains 1-3, K1-3.
 X W Human; plasminogen; angiostatin; neovascularisation;
 W kringle domain; cell proliferation; viral vector;
 W replication-defective; cancer; tumour.
 X S Homo sapiens.
 X N WO200288173-A2.
 X D 07-NOV-2002.
 X F 29-APR-2002; 2002WO-US13461.
 X X 30-APR-2001; 2001US-287673P.
 R 05-APR-2002; 2002US-370634P.
 X A (CELL-) CELL GENESIS INC.
 X Chang B, Wu WW, Macarthur J, Patel S, Jooss K, Mendez M,
 X WPI; 2003-129131/12.
 R N-PSDB; ABA00776.
 X New recombinant viral vector expressing human angiostatin useful for
 inhibiting angiogenesis in a mammalian subject with cancer or tumor -
 X Disclosure; Page 75-76; 83pp; English.
 | C This sequence represents kringle domains 1-3 of human plasminogen. A 38
 | C N-terminal fragment of plasminogen is referred to as angiostatin and
 | C inhibits neovascularisation. Angiostatin contains 4 kringle domains of
 | C the parent molecule. However, angiostatin containing all 4 kringle
 | C domains (K1-4) was found to be no more potent as an inhibitor of cell
 | C proliferation than an angiostatin only containing K1-3. Therefore,
 | C kringle 4 does not possess inhibitory activity. A fragment of the
 | C plasminogen coding sequence may be used in the recombinant viral vector
 | C of the invention for obtaining angiostatin activity. The vector
 | C comprises a promoter capable of expressing human angiostatin operably
 | C linked to a structural gene encoding one or more domains of human
 | C angiostatin. The vector, which may be a replication defective viral
 | C vector, is useful for inhibiting angiogenesis in a mammal, especially
 | C with cancer or a tumour.
 | X Sequence 260 AA;
 | 2 Query Match 39.9%; Score 712; DB 24; Length 260;
 | Best Local Similarity 42.3%; Pred. No. 1-6e-38;
 | Matches 129; Conservative 41; Mismatches 85; Indels 50; Gaps 7;
 | Y 5 VQDGHGGRGSRGTSSTIVTGTCQWSKTTPHQRPENPNAGLTYCNRPDSK 64
 | b 3 LSECKTGNGKNTFRGIMSKTKGTCQWSSTSPHRPRSPATHSEGEEYNCRNPNDP 62
 QY 65 Q-PWCYTIDPCVRYEYCNLTQCSFESGVLETPTVVPVSMEAHSEAPTEQTPVYQCY :::
 Db 63 QGPWCYTIDPCVRYEYCNLTQCSFESGVLETPTVVPVSMEAHSEAPTEQTPVYQCY :::
 QY 124 HGNQSYRGFRFSTIVTGTCQWSKTTPHQRPENPNAGLTYCNRPDSKADTGWCFC 183
 Db 90 HCGENDGKISKTMGLEQAWDOSOPHAGYIPSKEPNKLKNYCRNPDRLLRWCFC 149
 QY 184 TWDPSTRWEYCNLTQCSUTDGTIVYAPPTVQYPSLGPSEODCMNGCYGRKKAFTV 243
 Db 150 TWDPSTRWEYCNLTQCSUTDGTIVYAPPTVQYPSLGPSEODCMNGCYGRKKAFTV 195
 QY 244 GTPQCQEWAAQEPHRHSTFIPGTCNKWAGLEKNCRNPDQDINGPWCYTMMPRKLFDYCDIP 303
 Db 196 GTCQIWSACTOPHINR-TPENFPCKNLDENYCRNPDSK-RAPWCHTTSQVREYKIP 253
 QY 304 LGASS 308
 Db 254 SCDS 258

RESULT 11
 AAB01910
 ID AAB01910 standard; Protein; 274 AA.
 XX
 AC AAB01910;
 XX DT 18-SEP-2000 (first entry)
 XX DE Human plasminogen Kringles 1-3 (Tyr80-Pro353).
 XX KW Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiangiogenic; antiplatelet; antiatherosclerotic; cytoprotective;
 KW antipsoriatic; antinflammatory; antiulcer; anirheumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.
 XX OS Homo sapiens.
 XX PN US6057122-A.
 XX PD 02-MAY-2000.
 XX PP 05-MAY-1997; 97US-0851350.
 XX PR 03-MAY-1996; 96US-0643219.
 DR 03-APR-1997; 97US-0832087.
 XX PA (ABBO) ABBOTT LAB.
 XX PI Davidson DJ;
 XX DR WPI; 2000-349573/30.
 CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of

Page 8

endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human Plasminogen used in an exemplification of the invention.

Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in figure 1.

PT regions of plasminogen linked to the glycosylated form, useful for
 PT inhibiting angiogenesis -
 XX
 PS Claim 7: Fig 1; 42bp; English.
 XX
 CC The present sequence is deglycosylated kringle 1-5 region
 CC protein. Deglycosylated kringle 1-5 region protein has increased
 CC antiangiogenic activity as compared to glycosylated kringle 1-5 region
 CC protein. The deglycosylated kringle 1-5 region protein was isolated
 CC from human plasminogen by affinity chromatography.

Sequence	274 As;	39.9%;	Score 712;	DB 21;	Length 274;
Query Match	Y	Y	Y	Y	Y
Best Local Similarity	42.3%	Pred. No.	1.7e-38		
Matches	129;	Conservative	41;	Mismatches	85;
				Indels	50;
				Gaps	7;
5	VQDGTGNGSTRSISWSTTGRICQSNSMTPHRHORTPEVNPYNDGLTMVYCRNPDA	TGPNCF	64		
2	LSEKGTGKGKRNQTMKRGNSKTKQWQSSTSPHERPFPATHPSEELEYCNRPDDP	F 61			
65	Q-PNCYTIDPCVREYCNLTQCSETESGVLETPPTVPPSMSAEHSEAAPTEQTPVRCY	123			
62	QGPNCYTIDPCVREYCNLTQCSETESGVLETPPTVPPSMSAEHSEAAPTEQTPVRCY	123			
6	62 QGPNCYTIDPCVREYCNLTQCSETESGVLETPPTVPPSMSAEHSEAAPTEQTPVRCY	123			
6	62 QGPNCYTIDPCVREYCNLTQCSETESGVLETPPTVPPSMSAEHSEAAPTEQTPVRCY	123			
124	HGNCGOSYRGTFSTTIVGRICQSNSMTPHRHORTPEVNPYNDGLTMVYCRNPDA	DATGPNCF	183		
89	HCGSGNQYNGKISKRTMAGLEQANDSOSHARYIISKEPKNKKKNCRNEDRELRPCF	148			
184	TTDPSIREYKCNLUTRQLSDTGSTVAPPVIVQPSLQPPSQDGMFGNGKPGRKATIV	T 243			
149	TTDPSIREYKCNLUTRQLSDTGSTVAPPVIVQPSLQPPSQDGMFGNGKPGRKATIV	T 243			
0	TTDPKRNQELCDIPCT-----TPP-----TPP-----TPP-----TPP-----TPP	194			
244	GTPCOWEAQEPHRHSTFIFGTGNWAGLEKNTYCRNEDGTDINGPWCYDPRKLFDYCDIP	303			
195	GTCGSHAWAQQTPTHAK-TPEENFCNLDTCRNFDGK-TAPWCFPTNSQVREYCKP	252			
304	LCASS 308				
0	LCASS 308				
253	SCDS5 257				

Purifying recombinant angiostatin involves applying fermented broth containing angiostatin to expanded bed cation exchange column, exchange column, hydroxyapatite column, hydrophobic column and a membrane -

Example 1: Page 22; 49pp; English.

The present sequence representing Angiostatin protein is given in an invention providing a method for recombinant production, recovery and purification of Angiostatin protein. Purification of recombinant Angiostatin comprises applying crude fermentation broth containing the protein to an expanded bed cation exchange column, eluting it, and applying the eluate to anion exchange column, repeating the process of eluting and applying, to hydroxyapatite column, hydrophobic column and membrane, in order, and collecting fluid passing through the membrane. Angiostatin is useful for treating angiogenesis mediated diseases, including solid tumours, leukaemia, tumour metastases, benign tumours, rheumatoid arthritis, psoriasis, ocular antigenic diseases, Oster-Webber syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiofibroma and wound granulation. As a centrifugation technique is not employed in the process, damage to the cells with concomitant release of undesirable biological materials such as cytochromes, pigments, enzymes, chemicals and other undesirable cellular constituents and debris, is prevented. Large scale recovery and purification of proteins is greater than that obtained from prior art methods. Active Angiostatin can be stored in buffers for extended periods of time, in vials or other containers, either in solution which may be liquid or frozen, or lyophilised.

KW	vascular endothelial cell; ophthalmic disease; glaucoma;
KW	diabetic retinopathy; arthritis; psoriasis.
XX	
OS	Homo sapiens.
NN	WO961464-A1.
XX	
PD	02-DE5-1999.
XX	
PP	28-MAY-1999; 99WO-KR00263.
XX	
PR	28-MAY-1998; 98KR-0019535.
PR	27-MAY-1999; 99KR-0019144.
XX	
PA	(GREC) KOREA GREEN CROSS CORP.
XX	
PI	You WK, So SH, Ahn BC, Lee H, Jung S, Kim Y, Lee J,
PI	Joe YA, Chang S;
XX	
DR	WO1; 2000-086703/07.
XX	
PT	Purifying angiogenesis inhibitors produced as recombinant
PT	<i>Escherichia coli</i> , useful as anticancer agents and for tri-
PT	diseases -
XX	
PS	Claim 2; Page 47-48; 55pp; English.
XX	
CC	The present sequence represents the human greenstatin com-
CC	is derived from the plasminogen portion, and comprises an
CC	amino acid sequence.

amino acids 99-467. Angiotatin and greenstatin are used as thrombolytic factors and angiogenesis inhibitory proteins. Angiotatin contains the kringle 1-4 region of plasminogen, and greenstatin contains the kringle 1-3 region of plasminogen. As both proteins contain a high number of disulphide bonds, they are difficult to purify. The specification describes a method for the purification of such angiogenesis inhibitory proteins. The method comprises solubilising the proteins, produced as inclusion bodies in *Escherichia coli* and refolding the solubilised fraction in buffer containing urea and glutathione. The angiogenesis inhibitory proteins specifically inhibit proliferation of vascular endothelial cells, but not that of non-endothelial cancers or normal cells. The angiogenesis inhibitory proteins are used to suppress angiogenesis, specifically for treating cancers (e.g. lung, skin and brain), or ophthalmic diseases (e.g. glaucoma and diabetic retinopathy), but also arthritis and psoriasis.

Sequence	QY	Score 39.6%	Length 254;
Best Local Similarity	42.4%;	Pred. No. 3-3e-38;	
Matches	128; Conservative	Mismatches 40;	Indels 50; Gaps 7;
Db	7 DCYHGDDGSRSYRGISSTTVGRCTQWSNSMIPHWHTPENYGRNPLSGKQ - 65		
Db	2 EXKTGKNYRGTSKTKNGTICQNSSTSHPRESPATHPSEGLEENTCRNPNDPQG 61		
QY	66 PWCYTTPDPCVRWLEYCNLFOCTESGYLETPTVVPMSMEAHSAAEPTQFPPVRCYCG 125		
Db	62 PWCYTTPDPERKDTCILECEE -----		
QY	126 NGOSYRGTFSTWVGRTCOSWSSMTPHRHQRTPEYNPNGLTMNYCRNPDADTGWCFTT 185		
Db	89 SGNNYDOKISTMSLCEQWDQSPhAgytPSXPNNLNKENYCNPDELRWCFTT 148		
Db	186 DPSIRKEYCNLTCSRSDTGTWVAPPYIQLQPSLGGPSEODCMFGNGYRKKATVYTG 245		
QY	149 DDKRKFLCPRCT-----TTP ----- PSSGPTYQ -CLKGTYGNRYRNVATVSLGH 194		
Db	246 PQQWIAQEPRHSTFIPGTNKAGLEKNTCRNPDDINGPWCYTMPLRKEDYCDIPLC 305		
QY	195 TQWHSAQTPTHNR-TPEFNPKNLIDENICRNPDGK-RAPWHTINSQVWEYKSKIPSC 252		
Db	306 AS 307		

Db 253 DS 254
 Db 88 GENYDOKKISKTMAQLEQAWNSQPHAGYTPSKFKENKKENYCRNFDGEPRPACTED 147
 RESULT 15
 AAW07568 standard; protein: 250 AA.
 IX AAW07568:
 IC 22-JUN-1997 (first entry)
 X Rhesus kringle 1-3.
 X angiotatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 X macular degeneration; diabetic retinopathy.
 X Rhesus.
 X W09635774-A2.
 D 14-NOV-1996.
 X 26-APR-1996; 96WO-US05856.
 X 08-MAR-1996; 96US-0612788.
 R 26-APR-1995; 95US-0429443.
 R 22-FEB-1996; 96US-0605598.
 X (CHIL-) CHILDRENS MEDICAL CENT.
 X Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;
 X WPI; 1996 518662/51.
 X Use of angiotatin fragments or aggregates - for inhibiting
 T endothelial cell proliferation and treating angiogenesis-mediated
 T diseases, e.g. cancer, arthritis or diabetic retinopathy
 X Claim 4; Page 125-126; 203pp; English.
 C The invention relates to new methods and compositions for
 C inhibiting endothelial cell proliferation, using as active component
 C an angiotatin fragment, a combination of angiotatin fragments, or
 C aggregate angiotatin. The fragment is preferably derived from murine,
 C human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
 C kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
 C 1-4 or kringle 1-4BKTs protein. The aggregate angiotatin has a MoI. Wt.
 C of 45-65 kD and is derived from plasminogen fragment beginning at
 C approximately amino acid number 98 of murine, human, Rhesus, porcine or
 C bovine plasminogen. The active component can be used for treating
 C angiogenesis-mediated diseases such as cancer, arthritis, muscular
 C degeneration and diabetic retinopathy. It can also be used to develop
 C antibodies for use in diagnosis, detection and therapy.
 C The present sequence, Rhesus kringle 1-3, is a specific angiotatin
 C fragment which can be used in the invention, and represents amino
 C acids 6-255 of Rhesus angiotatin.
 X Sequence 250 AA;
 Y Query Match Similarity 39.4%; Score 704; DB 17; Length 250;
 Best Local Similarity 42.5%; Fred. No. 5.1e-38;
 Matches 127; Conservative 40; Mismatches 82; Indels 50; Gaps 7;
 C CYHGDGRSYRIGISSTTYGRCCOSSSM1PHQRIPENTPAGLUTENYCRNPD-GKGP 66
 C 1 CRGNGKRNTRGTSKRIGCQKVSSTSPHRFTSFATHPSSEEEENYCRNPDNGQGP 60
 Y 67 WCYTDPYCWENYCNLHQCTESTEGVLETPTVVPVSMEAHSEAAPTQTPVVRQYGN 126
 b 61 WCYTDPYCWENYCNLHQCTESTEGVLETPTVVPVSMEAHSEAAPTQTPVVRQYGN :
 b 127 GOSYRGTFSTPVGRTQCSWSSMMTPHRHRTOPENYPNDGLTMYCRNPDADIGPWCFTD 186

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:01:08 ; Search time 29 Seconds
(without alignments)
449.370 Million Cell updates/sec

Title: US-10-088-548-2
Perfect score: 1786
Sequence: KSPVWDDCHGDRSGRGS.....YTMNPRKLFYCDIPLCASS 308

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 282628

Minimum DB seq length: 0
Maximum DB seq length: 308

Post-processing: Maximum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/podata/1/1aa/5A_COMB.Dep:/*
 2: /cgn1_6/podata/1/1aa/5L_COMB.Dep:/*
 3: /cgn2_6/podata/1/1aa/5A_COMB.Dep:/*
 4: /cgn2_6/podata/1/1aa/6B_COMB.Dep:/*
 5: /cgn2_6/podata/1/1aa/6C_COMB.Dep:/*
 6: /cgn2_6/podata/1/1aa/backfile1.Dep:/*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query Match	Length	DB ID	Description
1	716	40.1	250	2	US-08-012-788-33
2	716	40.1	250	3	US-09-066-028-33
3	716	40.1	250	4	US-09-035-025-33
4	715	40.0	250	2	US-08-012-788-32
5	715	40.0	250	3	US-09-066-028-32
6	715	40.0	250	4	US-09-035-025-32
7	704	39.4	250	2	US-08-012-788-31
8	704	39.4	250	3	US-09-066-028-31
9	704	39.4	250	4	US-09-035-025-31
10	703	39.4	250	2	US-08-012-788-30
11	703	39.4	250	4	US-09-066-028-30
12	703	39.4	250	4	US-09-035-025-30
13	700	39.2	250	2	US-08-012-788-29
14	700	39.2	250	3	US-09-066-028-29
15	700	39.2	250	4	US-09-035-025-29
16	585	32.8	210	3	US-08-085-526-21
17	538	32.8	168	2	US-08-012-788-24
18	538	30.1	168	3	US-09-066-028-24
19	538	30.1	168	4	US-09-035-025-24
20	531	29.7	168	2	US-08-012-788-27
21	531	29.7	168	3	US-09-066-028-27
22	531	29.7	168	4	US-09-035-025-27
23	524	29.3	130	4	US-08-039-4
24	519	29.1	91	3	US-09-024-553-1
25	516	28.9	120	1	US-08-211-47-7
26	515	28.8	168	2	US-08-012-788-26
27	515	28.8	168	3	US-09-066-028-26

ALIGNMENTS

RESULT 1
US-08-612-788-33
; Sequence 33, Application US/08612788
; Patent No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sun, B. Kim Lee
TITLE OF INVENTION: Angiotatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS: 45
ADDRESSE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERRAL/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Bovine
IMMEDIATE SOURCE:
CLONE: K1-3
US-08-612-788-33

Query Match 40.1%; Score 716; DB 2; Length 250;
 Best Local Similarity 42.1%; Pred. No. 1.86-57;
 Matches 126; Conservative 43; Mismatches 80; Indels 50; Gaps 7;

Y CYHGDRGSRIGLSSTTYGTCOSWSSMTPWHORTPEAGLTYENCRNPDGSQ-P 66
 | :|:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Jb 1 CTKGNDQTYTGTAAKSGVTCQKWAATSPHPKSPKEPAGLENCRNPDNDNGP 60
 WYTTPCVCWEXONLTQSESESGVLETPVVPMSHEAHSAPTEQTPTVRCYHGN 126
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Jb 61 WCYTTPDKYDQDIPED------KCJHCS 87
 127 GSYRGTFESTTYGTCOSWSSMTPHRQHTPEAGLTYENCRNPDADTGWPWCFITD 186
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Jy 88 GENYEKIARTMSGRDCQAWDQSPhAHTPSKREPNKLNYCRNPDGEPRWPWCFITD 147
 187 PSTRWEYCNLURCSDETEGVAPPVTVQPSLGPSPEDCMENGKGYROKKATTGTP 246
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Jb 148 PKRWEFCDIPRCI-----TPP----PSGP--KYOCLKGTKNKGTVAYTESGHT 193
 247 COWAAQEPHRHSTPSTNKAHLERNYCRNPDGDINGPQYTTANPRKLFCDIPLC 305
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Jb 194 CORWSQTOPKHNR-TPENPKNLEENYCRNPDGE-KAPWCYTANSEVRWEETIPS 250
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 RESULT 2
 US-09-066-028-33
 ; Sequence 33, Application US/09066028
 ; Patent No. 6024688
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Micheal
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:

ORGANISM: Bovine
 IMMEDIATE SOURCE:
 CLONE: K1-3
 US-09-066-028-33
 Query Match 40.1%; Score 716; DB 37; Length 250;
 Best Local Similarity 42.1%; Pred. No. 1.8e-57;
 Matches 126; Conservative 43; Mismatches 80; Indels 50; Gaps 7;
 Qy 8 CYHGRDERSFRGIGSSTTYGTCOSWSSMTPHRQHTPEAGLTYENCRNPDGSQ-P 66
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 1 CKTGNSQTYRTGAETRSGVICQNSATEPHVKFSKEFKLAGIEENYCRPNDENG 60
 Qy 67 WCYTTPCVCWEXONLTQSCSESEGVLETPVVPMSHEAHSAPTEQTPTVRCYHGN 126
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 61 WCYTTPDKYDQDIPED------KCJHCS 87
 Qy 127 GSYRGTFESTTYGTCOSWSSMTPHRQHTPEAGLTYENCRNPDADTGWPWCFITD 186
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 88 GNYEKKIAKTMSGRDCQAWDQSPhAHTPSKREPNKLNYCRNPDGEPRWPWCFITD 147
 187 PSIRWYCNUTRCSDTESTVYAPPVTVQPSLGPSPEDCMENGKGYRKATTGTP 246
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 148 PKRWEFCDIPRCI-----TPP----PSGP--KYOCLKGTKNKGTVAYTESGHT 193
 Qy 247 COWAAQEPHRHSTPSTNKAHLERNYCRNPDGDINGPQYTTANPRKLFCDIPLC 305
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 194 CORWSQTOPKHNR-TPENPKNLEENYCRNPDGE-KAPWCYTANSEVRWEETIPS 250
 ; Sequence 33, Application US/09066028
 ; Patent No. 6024688
 RESULT 3
 US-09-335-325-33
 ; Sequence 33, Application US/09335325
 ; Patent No. 651439
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 O'Reilly, Micheal
 Cao, Yihai
 Sim, B. Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: Bovine
IMMEDIATE SOURCE:
CLONE: K1-3
SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Query Match 40.1%; Score 716; DB 4; Length 250;
Best Local Similarity 42.1%; Pred. No. 1.8e-57;
Matches 126; Conservative 43; Mismatches 80; Indels 50; Gaps 7;

y 8 CYHGDRSYRGSISSTVYGRTCOSWSMITHPHQRTPEVNPGILTENYCRNPDGKQ-P 66
b 1 CTKGNQTYRTGTTAETKGTVQKNSATSPHPVAFESPCKFPLAGILENCRNPNDNGP 60

y 67 WYTTDPCVWYEONLNTQCSSESGYLETPTVYVPSEAHSEAAPEQTQPVYQCHGN 126
b 61 WYTTDPCVWYEONLNTQCSSESGYLETPTVYVPSEAHSEAAPEQTQPVYQCHGN 87

y 127 GOSYRFTESTVYGRTCOSSESMTPHRQHTPEVNPGILTMNYCRNPDADTGWCFTTD 186
b 88 GENYEKIAKMTSGRSRDCQAWDSOPIAHSAGYITPSRFPNKLKNMYCRNPDGEPRWCFTTD 147

y 187 PSLRWEYCNTRCSDTGTCTVVAAPTVIQVPSLGPSEODCMFONGKCYRGKKAATVGTGP 246
b 148 PQKWRFCDFCDRCT-----TPK-----FSSGP-----KYQCLKLGTKNYGGTVWTEGHT 193

y 247 COEWAQEPHRHSTFIPGTNKWAGLPEQGKQYCRNPDGDINGPWCYTMNPKLFDYCDIPLC 305
b 194 CORWSQTPHKHNR-TOPENFPCKNLEENICRNPDGE-KAPWCYTINSEVRWEITCIPSC 250

RESULT 4
S-09-335-325-33
Sequence 32, Application US/08612788
Patient No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiotensin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Porcine
IMMEDIATE SOURCE:
CLONE: K1-3
US-08-612-788-32

Query Match 40.0%; Score 715; DB 2; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.2e-57;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;

Qy 8 CYHGDRSYRGSISSTVYGRTCOSWSMITHPHQRTPEVNPGILTENYCRNPDGKQ-P 66
Db 1 CTKGNQTYRTGTTAETKGTVQKNSATSPHPVAFESPCKFPLAGILENCRNPNDNGP 60

Qy 67 WYTTDPCVWYEONLNTQCSSESGYLETPTVYVPSEAHSEAAPEQTQPVYQCHGN 126
Db 61 WYTTDPCVWYEONLNTQCSSESGYLETPTVYVPSEAHSEAAPEQTQPVYQCHGN 87

Qy 127 GOSYRFTESTVYGRTCOSSESMTPHRQHTPEVNPGILTMNYCRNPDADTGWCFTTD 186
Db 88 GENYEKIAKMTSGRSRDCQAWDSOPIAHSAGYITPSRFPNKLKNMYCRNPDGEPRWCFTTD 147

Qy 187 PSLRWEYCNTRCSDTGTCTVVAAPTVIQVPSLGPSEODCMFONGKCYRGKKAATVGTGP 246
Db 148 PQKWRFCDFCDRCT-----TPK-----FSSGP-----KYQCLKLGTKNYGGTVWTEGHT 193

Qy 247 COEWAQEPHRHSTFIPGTNKWAGLPEQGKQYCRNPDGDINGPWCYTMNPKLFDYCDIPLC 305
Db 194 CORWSQTPHKHNR-TOPENFPCKNLEENICRNPDGE-KAPWCYTINSEVRWEITCIPSC 250

RESULT 5
US-09-066-028-32
Sequence 32, Application US/09066028
Patient No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiotensin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids

ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REFERENCE NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 32:
 LENGTH: 250 amino acids
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Porcine
 IMMEDIATE SOURCE:
 CLONE: K1-3

Query Match 40.0%; Score 715; DB 3; Length 250;
 Best Local Similarity 42.5%; Pct. Mismatches 81; Indels 50; Gaps 7;

US-09-325-32 SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Y 8 CYHGDGSYRGISSSTVTGRTCSWSSMIPHWHORTPENYPNAGLIENTCRNPDSG-KQP 66
 b 1 CKTGNGKMYRQTTSKTKSGVICOKWSVSSHPKYSPEKEPLAGLENTCRNPNDKEGP 60
 Y 67 WCYTIDPCVRYEYCNLTCSETESGYLETPTVYVPSMEAHEAATQCPVYRCYHGN 126
 b 61 WCYTIDPCVRYEYCNLTCSETESGYLETPTVYVPSMEAHEAATQCPVYRCYHGN 126
 Y 127 GOSYRGFESTVYTGRTCSWSSMIPHWHORTPENYPNGLTNNYCRNPDAADTGCWCFPTD 186
 Y 88 GEYVEGKISKMGECQWGSOSPHAGTLPSPKPNKLKANYCNPDEPWCWCFPTD 147
 b 187 PSTRWEYCNLTCSETESGYLETPTVYVPSMEAHEAATQCPVYRCYHGN 126
 b 148 PNRWERCDIFRCT-----TP-----PTSGPYQ--CLKGRENVRGTVSTASHT 193
 Y 247 CQEWAAOPPHRSHTLPGPNKAWGLEKNYCRNPDDINGPWCVTMNPKLDYCDIPLC 305
 b 194 CQWWSAQSPHKHRN-TOPENFPCKNLNEENYCRNPDSG-TAPWCYTDSEVRWDYKIPSC 250

ESUIT 6
 S-09-335-325-32
 Sequence Application US/09335325
 GENERAL INFORMATION:
 APPLICANT: Folkmann, M. Judah
 O'Reilly, Michael
 Cao, Yihai
 Sun, B. Kim Lee

TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335,325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>

RESULT 7
 US-08-612-788-31
 Sequence 31, Application US/08612788
 ; Patent No. 5831682
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkmann, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sun, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: U.S.
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/335,325
 ; FILING DATE: 17-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/612,788
 FILING DATE: EPOCH: 08/06/2003
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rhesus monkey
 IMMEDIATE SOURCE:
 CLONE: K1-3
 US-08-612-788-31

Query Match 39 4%; Score 704; DB 2; Length 250;
 Best Local Similarity 42.5%; Pred. No. 2.2e-56;
 Matches 127; Conservative 40; Mismatches 82; Indels 50; Gaps 7;

QY 8 CXYGDGSYRGSISSTVYGRTCOSWSMISHWORTPNYPNAGLITENCRNPD -GKQP 66
 Db 1 CKTGNGKNYRGTMMSKTRGTTGTCQRWSSTSPPRPTSEPAHNYCRNPDNGQGP 60

QY 67 WCYTTPCVERWYCNLTQSETESGVLPTPVVVPNSMEAHSEAPTEQTPTVYRQYHGN 126
 Db 61 WCYTTPPEEREDYCIDIPECED-----

QY 127 GOSYRGTFESTVYGRTCOSWSMITHWORTPNYPNADGPMCFWCFTD 186
 Db 88 GENYDGKISKTMSGLECAWDQSPPAHLGYPSKFPAKLKNYCRNPDGEPREWCFTD 147

QY 187 PSTRWEYCNLTCSDETEGVWAPPVYQPSLGLPSEQDCMFGNGKGRGKKATTWCTP 246
 Db 148 PNKRWECDIPRC-----TTP-----PSSGTYQ-CURGTGTYNQREDVATVSYHT 193

QY 247 COFWAAQEPHRHSTFIPSTPKTNKAGLEKNYCRNPDGDDINGPWCYTMAPRKLEDFDIPLC 305
 Db 194 CHGWSAQQTPTHNR-TPENPCKNLJENYCRNPDGE-KAPWCYTTSNSQWREYCKIPSC 250

RESULT 8
 US-09-028-31
 Sequence 31, Application US/09066028
 Patent No. 6034688

GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rhesus monkey
 IMMEDIATE SOURCE:
 CLONE: K1-3
 US-09-066-028-31

Query Match 39 4%; Score 704; DB 3; Length 250;
 Best Local Similarity 42.5%; Pred. No. 2.2e-56;
 Matches 127; Conservative 40; Mismatches 82; Indels 50; Gaps 7;

QY 8 CYHGDGSYRGSISSTVYGRTCOSWSMISHWORTPNYPNAGLITENCRNPD -GKQP 66
 Db 1 CKTGNGKNYRGTMMSKTRGTTGTCQRWSSTSPPRPTSEPAHNYCRNPDNGQGP 60

QY 67 WCYTTPCVERWYCNLTQSETESGVLPTPVVVPNSMEAHSEAPTEQTPTVYRQYHGN 126
 Db 61 WCYTTPPEEREDYCIDIPECED-----

QY 127 GOSYRGTFESTVYGRTCOSWSMITHWORTPNYPNADGPMCFWCFTD 186
 Db 88 GENYDGKISKTMSGLECAWDQSPPAHLGYPSKFPAKLKNYCRNPDGEPREWCFTD 147

QY 187 PSTRWEYCNLTCSDETEGVWAPPVYQPSLGLPSEQDCMFGNGKGRGKKATTWCTP 246
 Db 148 PNKRWECDIPRC-----TTP-----PSSGTYQ-CURGTGTYNQREDVATVSYHT 193

QY 247 COFWAAQEPHRHSTFIPSTPKTNKAGLEKNYCRNPDGDDINGPWCYTMAPRKLEDFDIPLC 305
 Db 194 CHGWSAQQTPTHNR-TPENPCKNLJENYCRNPDGE-KAPWCYTTSNSQWREYCKIPSC 250

RESULT 9
 US-09-335-325-31
 Sequence 31, Application US/09335325
 Patent No. 6521439

GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 O'Reilly, Michael
 Cao, Yihai
 Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

TITLE OF INVENTION: Angiotatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45

ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/03/066,028

FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/612,788

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.

REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126

TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids

TYPE: amino acid
SPANNEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
CLONE: X1-3
US-09-066-028-30

Query Match 39.4%; Score 703; DB 3; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 73; Gaps 7;

US-09-335-325-30

Query Match 39.4%; Score 703; DB 4; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 83; Gaps 7;

US-09-335-325-30

Query Match 39.4%; Score 703; DB 4; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 83; Gaps 7;

US-09-335-325-30

Query Match 39.4%; Score 703; DB 4; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 83; Gaps 7;

US-09-335-325-30

Query Match 39.4%; Score 703; DB 4; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 83; Gaps 7;

US-09-335-325-30

Query Match 39.4%; Score 703; DB 4; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 83; Gaps 7;

US-09-335-325-30

Query Match 39.4%; Score 703; DB 4; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 83; Gaps 7;

US-09-335-325-30

Sequence 30, Application US/09335325
Patent No. 6521439

GENERAL INFORMATION:
APPLICANT: Folkinan, M. Judah
O'Reilly, Michael
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiotatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: X1-3
US-09-066-028-30

Query Match 8 CYHDGDRYGRGGSSTVGTCTQWSSMIPWHQTPENYPNAGLTENYCRNPDSGKQ-P 66
DB 1 CKRGNGNRYRGMTCNTKGATCOKWSSPRSPNPAHSEAAPIEQTVVVRQCYHGN 126
DQ 67 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 68 GENYDGKSKMSKMGSLCQWDQSPEAHGYIPSKPKNPKKKYCRNPDRDLRPRCFID 147
DQ 127 GQSYRGFSSTVGTCTQWSSMIPWHQTPENYPNAGLTENYCRNPDSGKQ-P 66
DQ 69 1 CKTGNGNRYRGMTCNTKGATCOKWSSPRSPNPAHSEAAPIEQTVVVRQCYHGN 126
DQ 70 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 71 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 72 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 73 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 74 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 75 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 76 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 77 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 78 GENYDGKSKMSKMGSLCQWDQSPEAHGYIPSKPKNPKKKYCRNPDRDLRPRCFID 147
DQ 79 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 80 PSIRWECKNLTRCSDEGTIVAPPVQIOPSLGPSEQDPMFNGKGYRKAKTIVGTP 246
DQ 81 148 PNRKWECLDIPRCI-----TPP----PSSGGPYQ--CLKGTKGENYRGRVAVTWSGHT 193
DQ 82 247 CQEWAQBPQRPHRSHTFIPGTNKWAGLEKVNCRNPDSGIDINGPWCYTMMNPKLFDYCDIPIC 305
DQ 83 194 CQHNSAQTPHTHNR-TPENPKNLDENYCRNPDRGR-RAPFWCHTNTSQVRNEYCRIPS 250

RESULT 12
US-09-335-325-30
Sequence 30, Application US/09335325
Patent No. 6521439

Query Match 8 CYHDGDRYGRGGSSTVGTCTQWSSMIPWHQTPENYPNAGLTENYCRNPDSGKQ-P 66
DB 1 CKRGNGNRYRGMTCNTKGATCOKWSSPRSPNPAHSEAAPIEQTVVVRQCYHGN 126
DQ 67 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 68 GENYDGKSKMSKMGSLCQWDQSPEAHGYIPSKPKNPKKKYCRNPDRDLRPRCFID 147
DQ 69 1 CKTGNGNRYRGMTCNTKGATCOKWSSPRSPNPAHSEAAPIEQTVVVRQCYHGN 126
DQ 70 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 71 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 72 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 73 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 74 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 75 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 76 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 77 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 78 GENYDGKSKMSKMGSLCQWDQSPEAHGYIPSKPKNPKKKYCRNPDRDLRPRCFID 147
DQ 79 1 WCYTTDPCVREYCNCUQCSETESGVLETPTVVPVPSMEAHSEAAPIEQTVVVRQCYHGN 126
DQ 80 PSIRWECKNLTRCSDEGTIVAPPVQIOPSLGPSEQDPMFNGKGYRKAKTIVGTP 246
DQ 81 148 PNRKWECLDIPRCI-----TPP----PSSGGPYQ--CLKGTKGENYRGRVAVTWSGHT 193
DQ 82 247 CQEWAQBPQRPHRSHTFIPGTNKWAGLEKVNCRNPDSGIDINGPWCYTMMNPKLFDYCDIPIC 305
DQ 83 194 CQHNSAQTPHTHNR-TPENPKNLDENYCRNPDRGR-RAPFWCHTNTSQVRNEYCRIPS 250

RESULT 12
US-09-335-325-30
Sequence 30, Application US/09335325
Patent No. 6521439

RESULT 13
 US-08-612-788-29
 Sequence 29, Application US/08612788
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; STATE: Georgia
 ; CITY: Atlanta
 ; COUNTRY: U.S.
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Paintlin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612-788
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05213-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-7799
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 250 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Murine
 ; IMMEDIATE SOURCE:
 ; CLONE: K1-3
 ; US-08-612-788-29

Query Match 39.2%; Score 700; DB 2; Length 250;
 Best Local Similarity 41.1%; Pred. No. 5e-56;
 Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps 6;

Qy 8 CYHGDGRSRYGGSITVYGRTCQWSWMSIPTPHQRPENPAGLTENYCRNPDKO-P 66
 Db 1 CKTGIGNGYRCGMRSIKSGTACQKWAEPHPNTSPSHPNEGLEENYCRNPDNDEGP 60
 Qy 67 WCYTDPCKVWEFCNTLQCSETESGVLETPTVVPVPSMPAHSEAAPTEPVPVQCHGN 126
 Db 61 WCYTDPDKRYDCNPECE-----ECMYCS 87

Qy 127 GQSYTGTFTTYGRCQSISMPHRHQRTENTDGTNYCRIPTDAUTGPWCFTD 186
 Db 88 GEKYGKLSKTSGLQANDSQSPHAGYPAKFPSKNEKMYCHNPDGEPRWCFTD 147

Qy 187 PSIRGYCNLTCRSDTEGTVYAPPTVQPSLGPSEODMFNGKSYGRKGKATTGTP 246
 Db 148 PTKREYCDIPR-----PTPPPP-----PTSTYQCLKRGERYGTVSTVSGRT 193

Qy 247 CQEAAQEPHRHISTIPGTTNKWAGLEKNYCRNPDDINGPWCTMMRKLFDYCDIPIC 305

QY 187 PSIRWEYCNLTCRSDDETVIAPPVIQVPSLGPSEQDCMFNGKGRKKATVGTGTP 246
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 148 PTKEWEXCDIPRC----TTPPPP----PTPEKQCLKGSRGENYRGTVSRTVSGRT 193
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 247 CQEWAQSPHRHSTFLPGTINKWAGLEKNAVCRNPGLDINGPWCYTMNPKLFDYCDIPLC 305
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 194 CQRREQCTPHRHNR-TPENFPCRNLEENYCRNPDGE-TAPWCYTDSOLRNEYCIPSC 250
 :|:|||:|||:|||:|||:|||:|||:|||:|||:
 RESULT 15
 US-09-335-325-29
 ; Sequence No. 191, Application US/09335325
 ; Patent No. 6521139
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Juddah
 ; O'Reilly, Michael
 ; Cao, Yihai
 ; Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: U.S.
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy diskible
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/335,325
 ; FILING DATE: 17-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 052113-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-3799
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 250 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: -<Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Murine
 ; IMMEDIATE SOURCE:
 ; CLONE: K1-3
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-09-335-325-29

Query Match 39.2%; Score 700; DB 4; Length 250;
 Best Local Similarity 41.8%; Pred. No. 5e-56; Gaps 6;
 Matches 123; Conservative 37; Mismatches 89; Indels 50;

QY 8 CYHGDGRSYRGLSSTVTGTCOSWSMHPHQTPPEVNLNTYCRNPDSGKQ-P 66
 Db 1 CKTGIGNYRGTMSRKSGTACQKWGETPPHNSPSPHPRCILEENYCRNPNDEGP 60
 Qy 67 WCYTDPVCVNEYCNLTQCSSETESGVLETPTVVPVSNEAHSPEAPTEQPVVRQCYHN 126
 :|:|||:|||:|||:|||:|||:|||:|||:|||:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

September 29, 2003, 08:03:07 ; Search time 347 Seconds
(without alignments)
134.301 Million cell updates/sec

Sequence score: US-10-088-548-2
Sequence: 1 KSPVYQDCYTHGDSRYSRGIS.....YTNNPRKLFDYCDIPLCASS 308

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters: 373251

Minimum DB seq length: 0
Maximum DB seq length: 308

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications AA:
 1: /cgn2_6_ptodata/1/pubpaas/US07_PUBCOMB.pep.*
 2: /cgn2_6_ptodata/1/pubpaas/PCT_NEW_PUB.pep.*
 3: /cgn2_6_ptodata/1/pubpaas/US06_NEW_PUB.pep.*
 4: /cgn2_6_ptodata/1/pubpaas/US06_PUBCOMB.pep.*
 5: /cgn2_6_ptodata/1/pubpaas/US07_NEW_PUB.pep.*
 6: /cgn2_6_ptodata/1/pubpaas/PCTUS_PUBCOMB.pep.*
 7: /cgn2_6_ptodata/1/pubpaas/US08_NEW_PUB.pep.*
 8: /cgn2_6_ptodata/1/pubpaas/US08_PUBCOMB.pep.*
 9: /cgn2_6_ptodata/1/pubpaas/US09A_PUBCOMB.pep.*
 10: /cgn2_6_ptodata/1/pubpaas/US09B_PUBCOMB.pep.*
 11: /cgn2_6_ptodata/1/pubpaas/US09C_PUBCOMB.pep.*
 12: /cgn2_6_ptodata/1/pubpaas/US09_NEW_PUB.pep.*
 13: /cgn2_6_ptodata/1/pubpaas/US10A_PUBCOMB.pep.*
 14: /cgn2_6_ptodata/1/pubpaas/US10B_PUBCOMB.pep.*
 15: /cgn2_6_ptodata/1/pubpaas/US10C_PUBCOMB.pep.*
 16: /cgn2_6_ptodata/1/pubpaas/US10_NEW_PUB.pep.*
 17: /cgn2_6_ptodata/1/pubpaas/US60_NEW_PUB.pep.*
 18: /cgn2_6_ptodata/1/pubpaas/US60_PUBCOMB.pep.*

Database :
 Published Applications AA:
 1: /cgn2_6_ptodata/1/pubpaas/US07_PUBCOMB.pep.*
 2: /cgn2_6_ptodata/1/pubpaas/PCT_NEW_PUB.pep.*
 3: /cgn2_6_ptodata/1/pubpaas/US06_NEW_PUB.pep.*
 4: /cgn2_6_ptodata/1/pubpaas/US06_PUBCOMB.pep.*
 5: /cgn2_6_ptodata/1/pubpaas/US07_NEW_PUB.pep.*
 6: /cgn2_6_ptodata/1/pubpaas/PCTUS_PUBCOMB.pep.*
 7: /cgn2_6_ptodata/1/pubpaas/US08_NEW_PUB.pep.*
 8: /cgn2_6_ptodata/1/pubpaas/US08_PUBCOMB.pep.*
 9: /cgn2_6_ptodata/1/pubpaas/US09A_PUBCOMB.pep.*
 10: /cgn2_6_ptodata/1/pubpaas/US09B_PUBCOMB.pep.*
 11: /cgn2_6_ptodata/1/pubpaas/US09C_PUBCOMB.pep.*
 12: /cgn2_6_ptodata/1/pubpaas/US09_NEW_PUB.pep.*
 13: /cgn2_6_ptodata/1/pubpaas/US10A_PUBCOMB.pep.*
 14: /cgn2_6_ptodata/1/pubpaas/US10B_PUBCOMB.pep.*
 15: /cgn2_6_ptodata/1/pubpaas/US10C_PUBCOMB.pep.*
 16: /cgn2_6_ptodata/1/pubpaas/US10_NEW_PUB.pep.*
 17: /cgn2_6_ptodata/1/pubpaas/US60_NEW_PUB.pep.*
 18: /cgn2_6_ptodata/1/pubpaas/US60_PUBCOMB.pep.*

RESULT 1
US-19-761-120-33

; Sequence 33, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M., Judah
; ATTORNEY: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (33171-252068)
; CURRENT APPLICATION NUMBER: US/09-7761,120
; CURRENT FILING DATE: 2001-01-16
; PRIORITY NUMBER: 09/309,821
; PRIORITY FILING DATE: 1999-05-11
; PRIORITY APPLICATION NUMBER: 08/7866,735
; PRIORITY FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 33
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Bos sp.
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Kringle 1-3
US-09-761-120-33

SUMMARIES

8

result No.	Score	Query Match	Length	DB ID	Description
1	716	40.1	250	9 US-09-761-120-33	Sequence 33, Appl
2	716	40.1	250	10 US-09-761-120-33	Sequence 33, Appl
3	716	40.1	250	15 US-10-31-41-33	Sequence 33, Appl
4	715	40.0	250	9 US-09-761-120-32	Sequence 32, Appl
5	715	40.0	250	10 US-09-335-325-32	Sequence 32, Appl
6	715	40.0	250	15 US-10-31-41-32	Sequence 32, Appl
7	711	39.8	260	15 US-10-31-241-61	Sequence 61, Appl
8	704	39.4	250	9 US-09-761-120-31	Sequence 31, Appl
9	704	39.4	250	10 US-09-335-325-51	Sequence 31, Appl
10	704	39.4	250	15 US-10-31-41-31	Sequence 31, Appl
11	703	39.4	250	9 US-09-761-120-30	Sequence 30, Appl
12	703	39.4	250	10 US-09-335-325-30	Sequence 30, Appl
13	703	39.4	250	15 US-10-31-241-30	Sequence 9, Appl
14	700	39.2	250	9 US-09-761-120-29	Sequence 9, Appl
15	700	39.2	250	10 US-09-335-325-29	Sequence 9, Appl

Sequence 29, Appl
Sequence 21, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 25, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl

US-10-131-241-29
US-10-036-869-21
US-09-761-120-27
US-09-335-325-27
US-10-131-241-27
US-09-748-168-1
US-09-761-120-26
US-09-335-325-26
US-10-131-41-26
US-09-761-120-28
US-09-335-325-28
US-10-131-241-28
US-09-761-120-25
US-09-335-125-25
US-10-131-41-25
US-09-761-120-38
US-09-335-325-38
US-10-131-241-38
US-09-761-120-37
US-09-335-125-37
US-10-131-41-37
US-09-761-120-36
US-09-335-325-36
US-10-131-241-36
US-09-761-120-35
US-09-335-325-35
US-10-131-241-35

US-19-761-120-33

;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


```

; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 0534-A0151 (43171-25208)
; CURRENT APPLICATION NUMBER: US/09/761,120
; PRIORITY FILING DATE: 2001-01-16
; PRIORITY APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 32
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Sus sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 1-3
US-09-761-120-32

Query Match 40.0%, Score 715, DB 9, Length 250;
Best Local Similarity 42.5%, Fred. No. 9, e-5;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;

QY          8 CYHGDGRSTRGILSSTIVTGRICQSWSMMPHQRTPENPVNAGLTENYCRNPDSG-KQP 66
Db          1 CKTGNGKNTGRTSKSGVTCQKSVSPPHPKYSPEKPLAEENCRPDNEDKGP 60
QY          67 WCYTDPVCYRWCNLTOCSTESGYLEPTVVPVPSMEAHSEAAPTEQTPVYRCYHGN 126
Db          61 WCYTDPVCYRFDQDIEBCED-----ECMHCSC 87
QY          127 GQSYKRGTFESTIVTGRICQSWSMMPHQRTPENPVNAGLTENYCRNPDACTPQETTD 186
Db          88 GEHYEKGKLSKTMSGIEQSWSQSOSPHAGYLPSKEPKUNLMMCRNPDGEPRWCFTTD 147
QY          187 PSIRYEYCNTRCSDEGSTVAPPVIVQPSLQPPSQDCMFNGKGRKGKATTVGTP 246
Db          148 PNKRHEPCUDPRTC-----TPP-----PSSQGRENFGTYVTSAGT 193
QY          247 CQEAQAEOPHRHSTFIPGTNNKAGLEKNYCRNPDDGINGPWCTMNPRKLFDYCDIPLC 305
Db          194 CQRWSAQSPHKNR-TPENFCKNLBENYCRNPDG-E-TAPWCVTDSSEVRDDCKIPSC 250

RESULT 5
US-09-325-32
; Sequence 32, Application US/09335325
; Patent No. US/00216417A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; Cao, Yihai
; Sim, B. Kim Lee
; TITLE OF INVENTION: Angiotensin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/335,325

```

SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Porcine
; US-10-131-241-32

Query Match 40.0%; Score 715; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 9.4e-55;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;
Db 8 CYHGDRSYRGISSTTGTGTCOSWSSMIPHWHORTPENYNPAGLTTENYCRNPDSGK 66
Db 1 CTRGNKNYRGTTSKRSGYICQRWSYSSPHKPSPEKPLAGLEETNYCRNPDEKGK 60

Query Match 40.0%; Score 715; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 9.4e-55;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;
Db 67 WCXTTDPCVREYCNLCTCSETSGVLETPVYVPSMEAHSAAPIEQTVYRCYHGN 126
Db 61 WCXTTDPCATRFYCDIPECED-----ECMBCS 87

Query Match 40.0%; Score 715; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 9.4e-55;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;
Db 127 GQSYRGPESTTYGRTQCQSSMTPHQRTPENYDADTGPNCFPTD 186
Db 88 GEHYEKRISKTMMSGTFCQSWGSQSPHAEGYLPSKTFNKNKMYCRNEDGERPNCFTD 147

Query Match 40.0%; Score 715; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 9.4e-55;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;
Db 187 PSTRWYCNLPRCSDFTEGVAPPVYQPSLGPSEDMFGNGKGRGKATTVGTG 246

Query Match 40.0%; Score 715; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 9.4e-55;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;
Db 148 PNKRWEFCDIRCT-----TPP-----PSGPIYQ---CLKGRGENYRGTIVSFTASHT 193

Query Match 40.0%; Score 715; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 9.4e-55;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;
Db 247 CQWAAEPHRHSTTGTGTCOSWNLKFLFYCDIPLC 305

Query Match 40.0%; Score 715; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 9.4e-55;
Matches 127; Conservative 41; Mismatches 81; Indels 50; Gaps 7;
Db 194 CQRWAQSPHKHNR-TPENFPCRNLENYCRNPDEGE-TAFWCXTTDSEVRNDYCKIPSC 250

RESULT 7
US-10-131-241-61
; Sequence 61, Application US/10/131241
; Publication No. US2003012792A1
; GENERAL INFORMATION:
; APPLICANT: Holiday, John W.
; ATTORNEY: Fortier, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; FILE REFERENCE: 05/13-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131-241
; PRIOR APPLICATION NUMBER: US 08/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/085,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-131-241-61

Query Match 39.8%; Score 711; DB 15; Length 260;
Best Local Similarity 42.3%; Pred. No. 2.2e-54;
Matches 129; Conservative 40; Mismatches 86; Indels 50; Gaps 7;
Db 5 VQDCHGDGRSYRGISSTTGTGTCOSWSSMIPHWHORTPENYNAGLTENYCRNPDSGK 64
Db 3 LSECTGNKGNTGTMKSKTNGTICQKWSSTSPEARFSEPAHSEAPTEQPYVYOCY 123

Query Match 39.8%; Score 711; DB 15; Length 260;
Best Local Similarity 42.3%; Pred. No. 2.2e-54;
Matches 129; Conservative 40; Mismatches 86; Indels 50; Gaps 7;
Db 65 Q-PGCTTDPCVREYCNLCTCSETSGVLETPVYVPSMEAHSAAPIEQTVYRCYHGN 123
Db 63 QGPCTTDPCERYCDIPECED-----ECM 89

Query Match 39.8%; Score 711; DB 15; Length 260;
Best Local Similarity 42.3%; Pred. No. 2.2e-54;
Matches 129; Conservative 40; Mismatches 86; Indels 50; Gaps 7;
Db 124 HGNGOSYRGISSTTGTGTCOSWSSMIPHWHORTPENYNAGLTENYCRNPDAEGPCC 183
Db 90 HCSGENTDGKISKTMGLEQANDQSPhAHGyPSKFPNKLKKNYCRNPDRLEPwC 149

Qy 184 TIDPSIRWEYCNLCTCSETSGVLETPVYVPSMEAHSAAPIEQTVYRCYHGN 243
Db 150 TIDPNKREWLCDFPRCT-----TPP-----PSGGPYQ---CLKGTGENYRBDVATVSSHT 195

Qy 244 GTPCQEWAAEPHRHSTTGTGTCOSWNLKFLFYCDIP 303
Db 196 GHTCQHWASACTPHTER-TPENFPCRNLDENYCRNPDSK-RAPWCHTNNSQFWYCKIP 253

Qy 304 LCASS 308
Db 254 SCDS5 258

RESULT 8
US-09-761-120-31
; Sequence 31, Application US/09/61120
; Patent No. US200302037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; ATTORNEY: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 0940-0151 (43171-252068)
; CURRENT APPLICATION NUMBER: US/09/761-120
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/7309,821
; PRIOR FILING DATE: 1999-05-11
; PRIORITY: 08/8666,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Macaca sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 1-3
; US-09-761-120-31

Query Match 39.4%; Score 704; DB 9; Length 250;
Best Local Similarity 42.5%; Pred. No. 8.6e-54;
Matches 127; Conservative 40; Mismatches 82; Indels 50; Gaps 7;
Db 8 CYHGDRSYRGISSTTGTGTCOSWSSMIPHWHORTPENYNAGLTENYCRNPDS-GEQP 66
Db 1 CKTGNCNKNTGTMKSKTNGTQKWSSTSHPSEGLENYCRNPDPNDGQGP 60

Qy 67 WCYTDDPCVREYCNLTCSETSGVLETPVYVPSMEAHSAAPIEQTVYRCYHGN 126
Db 61 WCYTDDPCERDIDCIPCED-----ECM 87

Qy 127 GOSYRGFESTTGTGTCOSWSSMTPHRHQTPEYNPNDGLTANYCRNPDAEGPWCFTD 186
Db 88 GENYDKRISKTMSCLECAWDQSPhAHGyPSKFPNKLKKNYCRNPDRPEPWCFITD 147

Qy 187 PSIRWEYCNLCTCSETSGVLETPVYVPSMEAHSAAPIEQTVYRCYHGN 246
Db 148 ENKREWLCDFPRCT-----TPP-----PSGGPYQ---CLKGTGENYRBDVATVSSHT 193

RESULT 9
US-09-335-325-31
; Sequence 31, Application US/09/335325
; Patent No. US200216417A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; ATTORNEY: O'Reilly, Michael
; Cao, Yihai

Sim, B., Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335,325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-7799
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rhesus monkey
 IMMEDIATE SOURCE:
 CLINE: K1-3
 SEQUENCE DESCRIPTION: SEQ ID NO: 31:
 US-09-335-325-31
 Query Match Score: 704; DB: 10; Length: 250;
 Best Local Similarity: 42.5%; Pred. No.: 8.6e-54;
 Matches: 127; Conservative: 40; Mismatches: 82; Indels: 50;
 QY 8 CTHGDGRSYRGISSITVTGRTCCQSWSSMIPHWQHPTPNYPNAGLTENTCRNPD
 Db 1 CKTGNGKRYRGTMSKTRGITCOKWSSTPRPTFSATHPSEGGEENCRNDN
 QY 67 WCYTTDTCVREYCMILTCQCSSEFGVLETSTVYVPSMEASIAAPTEQTPTVRC
 Db 61 WCYTTDCEERDIDPEED-----Ev
 QY 127 GQSTURGFSTTVYGTQCSWSSMTPHRHPTPNYPNGLTMNYCENPDADEPPW
 Db 88 GENEYDGILKSTKMSIGECLQCWAQDSOPRAHGTIPSFPKNKKNNYCRNPDPGEPPW
 QY 187 PSIRWEYCNLTRCSDEGTIVVAPPVYQVPSLGPSPSEQDCMFNGKGYRKETT
 Db 146 PNRKWLWDLFRC-----TPP----PSSGGTYQ---CLKGIGENYRGDVAVT
 QY 247 CQEEAAQEPHHHSFIPGPKNAAGLEKNCRNPDGQDINGPRXYTNPRLIEDCD
 Db 194 CHGWSAQTPTHINR-TPENFCPKLDENYCRNPDPGE-KAPWCYTNSQVRWECK
 RESULT 10
 US-10-131-241-31

US-09-761-120-30

Query Match 39.4%; Score 703; DB 9; Length 250;
Best Local Similarity 42.5%; Pred. No. 1..1e-53;
Matches 127; Conservative 39; Mismatches 83; Indels 50; Gaps 7;

QY 8 CYHGDGSYRGISSSTVGRTCQSWSMIPHMQRTPEPNPAGLTTENCRNPDSGKQ-P 66
Db 1 CKTGNGNRYRTMSKTKNGTICKWSSSPRREPAPTHSELENYCRNPDDPQSP 60

QY 67 WCYTTPDPOVREYCNCQSETESGVLETPTVPPVPSMRHSEAPTRQTPVVRQYHGN 126
Db 61 WCYTIDDEKRDYCDILEEE-----

QY 127 GOSYRGFTSTVGRTCOSWSMTPHRORTPEPNPAGLTTENCRNPDDPQSP 60

Db 88 GENIDGTSKTMGSLCQAWDSDSPHAGY.LPSKPNKNKKNCRNFDRELRPCFTD 147

QY 187 PSTRWETONLTRCSDETEGVAPPVTVQPSLGPSEODCMFGNGKGRGKATVTTGTP 246

Db 148 PNKRWELCDIPRCT-----TPP-----PSSGTYQ--OLKGENGVRGNAVTVSGR 193

QY 247 COEWAQEPHRHSTFLPGTNKAGLEKKNCRNPDPGDINGPWCYTMNPFKLPYCDIPLC 305

Db 194 COHWSAQTPHTNR-TPENFPCNLDENYCRNPDSK-RAPWCHTNSQVNEYCKIPSC 250

RESULT 12

US-09-335-325-30

Sequence 30, Application US/09335325
Patent No. US2002014717A1

GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
ADDRESS: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3799
TELEFAX: 404-818-3799
INFORMATION FOR DOCKET NUMBER: 05213-0126

SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-09-335-325-30

FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1-3
SEQUENCE DESCRIPTION: SEQ ID NO: 30;

Query Match 39.4%; Score 703; DB 10; Length 250;
Best Local Similarity 42.5%; Pred. No. 1..1e-53;
Matches 127; Conservative 39; Mismatches 83; Indels 50; Gaps 7;

QY 8 CYHGDGSYRGISSSTVGRTCQSWSMTPHRORTPEPNPAGLTTENCRNPDSGKQ-P 66
Db 1 CKTGNGNRYRTMSKTKNGTICKWSSSPRREPAPTHSELENYCRNPDDPQSP 60

QY 67 WCYTTPDPOVREYCNCQSETESGVLETPTVPPVPSMRHSEAPTRQTPVVRQYHGN 126
Db 61 WCYTIDDEKRDYCDILEEE-----

QY 127 GOSYRGFTSTVGRTCOSWSMTPHRORTPEPNPAGLTTENCRNPDDPQSP 60

Db 88 GENIDGTSKTMGSLCQAWDSDSPHAGY.LPSKPNKNKKNCRNFDRELRPCFTD 147

QY 187 PSTRWETONLTRCSDETEGVAPPVTVQPSLGPSEODCMFGNGKGRGKATVTTGTP 246

Db 148 PNKRWELCDIPRCT-----TPP-----PSSGTYQ--OLKGENGVRGNAVTVSGR 193

QY 247 COEWAQEPHRHSTFLPGTNKAGLEKKNCRNPDPGDINGPWCYTMNPFKLPYCDIPLC 305
Db 194 COHWSAQTPHTNR-TPENFPCNLDENYCRNPDSK-RAPWCHTNSQVNEYCKIPSC 250

RESULT 13

US-10-131-241-30

Sequence 30, Application US/10131241
Publication No. US20030012792A1

GENERAL INFORMATION:
APPLICANT: Follett, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43110-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65
SEQ ID NO: 30

LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens

US-10-131-241-30

Query Match 39.4%; Score 703; DB 15; Length 250;
Best Local Similarity 42.5%; Pred. No. 1..1e-53;
Matches 127; Conservative 39; Mismatches 83; Indels 50; Gaps 7;

QY 8 CYHGDGSYRGISSSTVGRTCQSWSMTPHRORTPEPNPAGLTTENCRNPDSGKQ-P 66
Db 1 CKTGNGNRYRTMSKTKNGTICKWSSSPRREPAPTHSELENYCRNPDDPQSP 60

QY 67 WCYTTPDPOVREYCNCQSETESGVLETPTVPPVPSMRHSEAPTRQTPVVRQYHGN 126
Db 61 WCYTIDDEKRDYCDILEEE-----

QY 127 GOSYRGFTSTVGRTCOSWSMTPHRORTPEPNPAGLTTENCRNPDDPQSP 60

Result No.	Score	Query Match	Length	DB ID	Description
1	620	34.7	169	2 A40522	Plasmin (EC 3.4.21.21)
2	413	23.1	120	2 E61515	Plasmin (EC 3.4.21)
3	403	22.8	123	2 C61545	Plasmin (EC 3.4.21)
4	354	19.8	89	2 A60140	Plasmin (EC 3.4.21)
5	246.5	13.8	291	2 I38098	c-Plasminogen activator
6	88.5	5.0	277	2 I37552	c440 homolog - human
7	88.5	5.0	289	2 AB1075	right origin-blind
8	87.5	4.9	221	2 A47387	24K androgen-depen-
9	86.5	4.8	297	2 JQ1209	attachment protein
10	85.5	4.8	272	2 AB3430	transposase_BMII4
11	84.5	4.7	241	2 A85231	hypothetical protein
12	84.5	4.7	304	2 T24703	hypothetical protein
13	83.5	4.7	297	2 JQ1208	attachment protein
14	82	4.6	240	2 T33658	hypothetical protein
15	81	4.5	248	2 T19913	hypothetical protein
16	80	4.5	295	2 JC5559	Lectin B - Virginia
17	79.5	4.5	194	2 JC4559	immunoreactive protein
18	79.5	4.5	301	2 D44355	Cb4 glycoprotein
19	79	4.4	221	1 S24328	glutathione peroxidase
20	78.5	4.4	197	2 B49247	protozoite surface
21	78.5	4.4	287	2 S65765	chitinase (EC 3.2.1.2)
22	78	4.4	270	2 A13110	conserved hypothetical protein
23	78	4.4	270	2 C98176	lectin B - Virginia
24	77.5	4.3	104	2 S26415	immunoreactive protein
25	77.5	4.3	201	2 S24327	Cb4 glycoprotein
26	77	4.3	284	2 H87524	glutathione peroxidase
27	76	4.3	166	2 H89044	hypothetical protein
28	75.5	4.2	292	1 MGNZ60	protein B038-12
29	75.5	4.2	306	2 T52305	major surface glyc

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	30	75	4.2	127	2 S01286	whey acidic protein
OM protein - protein search, using sw model	31	75	4.2	221	2 B40464	glutathione peroxidase
Run on: September 29, 2003, 08:01:08 ; Search time 19 Seconds (without alignments)	32	75	4.2	243	2 A45854	common a
Perfect score: 1786	33	74.5	4.2	224	1 T28802	hypothetical prote
Sequence: 1 KEPVVVDCYHGGDRGSYRGTS.....YTMMPRKLFDYCIDIPLCASS 308	34	74	4.1	271	2 B40850	secretory protein
Scoring table: BLOSUM62	35	74	4.1	102	2 S29584	myo-inositol estab
Searched: 283308 seqs, 96168682 residues	36	73.5	4.1	104	2 S29592	Ig kappa chain V r
Total number of hits satisfying chosen parameters: 160415	37	73.5	4.1	108	2 S29581	Ig kappa chain V r
Minimum DB seq length: 0	38	73.5	4.1	262	2 T33597	hypothetical prote
Maximum DB seq length: 308	39	73.5	4.1	269	2 AH3580	iG lambda protein [imp
Post-processing: Maximum Match 0%	40	73.5	4.1	292	1 MGNZ18	major surface glyc
Database : PIR_76.*	41	73.5	4.1	206	2 A45517	coccidiolosis relate
1: pir1.*	42	73	4.1	86	2 S26458	hypothetical prote
2: pir2.*	43	73	4.1	86	2 S26459	Ig kappa chain V r
3: pir3.*	44	72.5	4.1	86	2 S29587	Ig kappa chain V r
4: pir4.*	45	72.5	4.1	86	2 S29587	Ig kappa chain V r
RESULT 1						ALIGNMENTS
A0522						
plasmin (EC 3.4.21.7) precursor - rat (fragment)						
C:Species: Rattus norvegicus (Norway rat)						
C:Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999						
C:Accession: A40522						
R:Kanatas, J.J.; Makker, S.P.						
J. Biol. Chem. 266, 10825-10828, 1991						
A:Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor						
A:Reference number: A40522; MUID:91250378; PMID:1645711						
A:Accession: A40522						
A:Status: preliminary						
A:Molecule type: mRNA						
A:Residues: 1-169 <RAN>						
A:Cross-references: GB:M62832; NID:9206215; PID:AAA41884.1; PID:g554488						
A:Note: the authors translated the codon TCT for residue 76 as Ala						
C:Superfamily: Plasmin; kringle homology; Plasminogen-related Protein precursor homolog						
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase						
F:34-112/Domain: kringle homology <KRG>						
F:34-112,55-95,83-107/Bisulfide bonds: #status predicted						
Query Match	34.7%	Score 620;	DB 2;	Length 169;		
Best Local Similarity	61.0%	Pred. No. 5.1e-39;				
Matches 111; Conservative	14;	Mismatches 43;				
Indels 14;		Gaps 2;				
QY	76	RWEYCNLTCQSETESGNGLETPTVVPVPSMBAHPAPPEQFPPVVRQCYHNGQSRTGFS	135			
	1	WYEYCHIPSQGSSVSPPDOSDSSVLP-----EQ1FPVYQCYXQGNGNSYRTGS	47			
Db	136	TTVTGRTCQWSMTHPRHRQHTPENYPNDGLTMNYCRPDAD-TGEWCFTTDPSIRWYC	194			
QY	1	TTNTGKQCQWVSTPFSKTPANEPSLSEMYCRPDNDQRGEWCFTTDPSVRYEC	107			
Db	195	NITRCSDTEGVYAPPITYQPSLGPSEODCMFGNGGYRKKAATVTCPOEWAAQE	254			
QY	108	NIKRKEETGGVAVSATVQPOPSAPTSEDCAGNGEYRKATAATPCQEWAAQE	167			
Db	255	PH 256				
QY	166	PH 169				
Db	168	PH 169				
RESULT 2						
Plasmin (EC 3.4.21.7) precursor - dog (fragments)						
N:Alternate names: Plasminogen						
C:Species: Canis lupus familiaris (dog)						
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995						
C:Accession: E61545						
R:Schaller, J.; Richtli, E.E.						
Enzyme 40, 63-69, 1988						
A:Title: Structural aspects of the plasminogen of various species .						

A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Accession: E61545
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-120 <C>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
F;37-114/Domain: kringle homology <KR4>

Query Match 23.1%; Score 413.; DB 2; Length 120;
Best Local Similarity 74.7%; Pred. No. 7_1e-24;
Matches 65; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 119 VRQCHNGGOSYRFTSTVGRICWSNTTPHRQTPENYPNPDGLTMNYCRNPDAAT 178
Db 34 VQECTHGNGGOSYRFTSTVGRICWSNTTPHRQTPENYPNPDGLTMNYCRNPDAK 93

RESULT 3
C61545 Plasmin (EC 3.4.21.7) precursor - goat (fragments)
N;Alternative names: Plasminogen
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
R;Schaller, J.; Rickli, E.E.
E;Enzyme 40; 63-69; 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Accession: C61545
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <C>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
F;41-118/Domain: kringle homology <KR4>

Query Match 22.0%; Score 408; DB 2; Length 123;
Best Local Similarity 73.9%; Pred. No. 1.7e-23;
Matches 68; Conservative 9; Mismatches 13; Indels 2; Gaps 1;

QY 110 AAPTECPTPVYCHNGGOSYRFTSTVGRICWSNTTPHRQTPENYPNPDGLTMN 169
Db 31 AAKCEEE- AODCTHNGQSFRTGTSSTVTRGKCSWSSMIPHRQTPESYNAGLMN 88

QY 170 YCRNPDAATGDPWCRTDPSIRVEYCNULTRCSD 201
Db 89 YCRNPDAKSPWCYTDTDRVRWEFCNLKCSE 120

RESULT 4
A60140 Plasmin (EC 3.4.21.7) precursor - chicken (fragment)
N;Alternative names: Plasminogen
C;Species: Gallus gallus (chicken)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
R;Groves, M.; Petty, L.
Biochim. Biophys. Acta 832, 326-330, 1985
A;Reference number: A60140; MUID:86077796; PMID:4074753
A;Accession: A60140
A;Molecule type: protein
A;Residues: 1-89 <C>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
F;6-83/Domain: kringle homology <KR5>
F;6-83/27-66; 55-78/Disulfide bonds: #status predicted
F;39/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.8%; Score 354; DB 2; Length 89;
Best Local Similarity 67.9%; Pred. No. 1.2e-19;
Matches 55; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 121 QCYHGNQGSYRFTSTVGRICWSNTTPHRQTPENYPNPDGLTMNYCRNPDAATGP 180
Db 5 ECYQGNQGSYRFTSTVGRICWSNTTPHRQTPENYPNPDGLTMNYCRNPDAATGP 184

QY 181 WCFITDPSIRVEYCNULTRCSD 201
Db 65 WCYITDPSYRVEYCNULTRCSD 85

RESULT 5
I38098 t-plasminogen activator precursor, inactive endothelial splice form - human
N;Alternative names: tissue plasminogen activator
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 22-Jun-1999
C;Accession: I38098; S01678
R;Siebert, P.D.; Fong, K.
Nucleic Acids Res. 18, 1066, 1990
A;Title: Variant tissue type plasminogen activator (PLAT) cDNA obtained from human en
A;Accession: I38098
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-291 <S>
A;Cross-references: ENBIL:X13097; NID:935282; PID:CAA1489.1; PMID:1969145
A;Comment: For the main splice form, see EIR:UKHTU. This form probably does not have
C;Genetics:
A;Gene: GDB:PLAT
A;Cross-references: GDB:119496; OMIM:173370
A;Map position: 8p12-p12
A;Intron positions: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
C;Keywords: alternative splicing; fibrinolysis; glycoprotein; kringle
F;1-23/Domain: signal sequence #status Predicted <S>
F;1-24-32/Domain: propeptide #status Predicted <PRO>
F;33-291/Domain: t-plasminogen activator inactive endothelial splice form #status P
F;41-78/Domain: fibronectin-type I repeat homology <EGF>
F;86-119/Domain: EGF homology <EGF>
F;1127-208/Domain: kringle homology <KR1>
F;115-291/Domain: kringle homology #status atypical <KR2>
F;41-71, 69-78, 86-97, 91-108, 110-119, 127-208, 148-190, 179-203/Disulfide bonds: #status P
Query Match 13.8%; Score 246.5; DB 2; Length 291;
Best Local Similarity 26.2%; Pred. No. 3.7e-11;
Matches 80; Conservative 34; Mismatches 110; Indels 81; Gaps 14;

QY 14 RSYRGI--SSVTIVRWCN--LTQCSSETESGVLETIVPPVPSMEAHSEAATPTECPTPVYCHNGQ 70
Db 35 RSYQVICDEKTONITQHQSWLRLPVL SRVVEYCNUCNAGRACHSYVPPVKCSERFCN 93

QY 71 TDPVCYRWCN--LTQCSSETESGVLETIVPPVPSMEAHSEAATPTECPTPVYCHNGQ 128
Db 94 GGTGQALYFSDEVCOPPEFG --KCCBIDRAT-----CYDDQGI 133

QY 129 SYRFTSTVGRICWSNTTPHRQ--RTPENYPNPDGLTM---NYCRNPDAATGP 180
Db 134 SYRFTWSTAESGAECINWNNSALAQNAYSGRP----DATRLGQNLNYCRNPDDSKP 188

QY 181 WCFITDPSIRVEYCNULTRCSDGTGTVAPPVIVQPSLQPPSHQDFGNFRGTRGKKA 239
Db 189 WCYTFKAKSYSEFCPTPASE----GNSDCYFGNSAFTGTHS 228

QY 240 TTYVGTGPGQEW-----AAQEPHRHSTFIPGTNKWAGLER-NYCRNPDDGINGPNC 288
Db 229 LTEGASCLPNMSMILLGKVTAONPSQA-----LGLGRHNCRT-GRSYSSPAT 278

QY 289 YTMAP 293

Db	279 ASMRP 283	Db	97 SQTBALYRRSPPEWSARGIRPLRLGEFFTVPEHQFTVLEDPLGLWTQSTS-----146
RESULT 6		QY	68 CTFDPCTYRWEIQCNTLQCSSETESGVV-----ETPTVPPV-----PSMEAHSF 109
I37552	OX10 homolog - human	Db	147 -----CSLEQISDFRHMRVQFWHDFLGHSPITPPVLYGLNETRPSMEKDDQ 194
C;Species: Homo sapiens (man)	C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000	QY	110 -----AAPTEQT-----PVYRQ-----CYRNGSYRTEFSTVTTVORTCWSWS 148
C;Accession: I37552	R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat	Db	195 EVFTTAAHQTPEADGTVQASHAPVLLQGEYVIMTYFSLGCVQ DFLIVYV-TCMPMN 252
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat	Eur. J. Immunol. 24, 677-683, 1994	QY	149 MTPHRHQRTPEVNPNDGTMNYCRNPDAATG 179
A;Title: The human OX10 homolog: cDNA structure, expression and chromosomal assignment	A;Reference number: I37552; MUID: 94170844; PMID: 7510240	Db	253 LTRRKQDQDTERYPE-----DIRKTG 273
A;Accession: I37552	A;Status: preliminary; translated from GB/ENBL/DBJ		
A;Molecule type: mRNA			
A;Residues: 1-277 <RES>			
A;Cross-references: EMBL:X75962; NID:942957; PIDN:CAA53576..1; PID:9472958			
C;Superfamily: CD27 antigen; NGF receptor repeat homology			
Query Match Score 5.0%; Score 88.5; DB 2; Length 277;			
Best Local Similarity 19.0%; Pred. No. 17;			
Matches 51; Conservative 31; Mismatches 89; Indels 97; Gaps 12;			
QY 18 GRSSTVIGTC--QSWSSMIIHWQHTPENYPNAGLLENYCRNPDSGKOPWC-----68			
Db 20 GUIGLSWYTGHCYGDITYSNSDCKCHCRPN---GKYSRCPSQNVCP-CCGPFYND 74			
QY 69 -YTTDPVCVRNEYCNLTOCSETESGVLETPTVY-----PVPSMAHSEAPTEQTPTVY 119			
Db 75 VVSSPKPCKPTCWNRSSSERKOLCATQDTIVCRAGTQPLDSYKRGVDACPAPP----130			
QY 120 RQYHNGQSYRGTSTYVTGTCQWSMSMT-PHQRHQTPEVNPNGLTMNYCRNPDAAT 178			
Db 131 -----GHSPPG-DNQACKPTINCTLAGHTLQPAHNSSDAI-----165			
QY 179 GPWNCFTTDPSLRWEIICNLTRSDTGGTAVVAPPVILQVPLGPSEQDMFGNGKSYRKK 238			
Db 166 -----CDRD-----PPATQPKQGP-----183			
QY 239 ATIVTGTPCQEW--AAQEPHRHSTFPIG 264			
Db 184 ARPTIVQPTEAWPRTSQGPSTRPVEVFG 211			
RESULT 8			
AB105 right origin-binding protein [imported] - Salmonella enterica subsp. enterica serovar Ty			
C;Species: Salmonella enterica subsp. enterica serovar Typhi			
C;Note: This species has also been called Salmonella typhi			
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002			
C;Accession: AB105			
R;Doughan, G.; James, K.D.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Geora, P.			
Nature 413, 848-852, 2001			
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;			
A;Title: Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serov			
A;Reference number: AB0502; MUID: 21534947; PMID: 11677608			
A;Accession: AB1075			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-289 <PAR>			
A;Cross-references: GB:AL513382; PIDN:CAD03417..1; PID:g16505685; GSPDB:GN00176			
C;Genetics: STR4933			
Query Match Score 5.0%; Score 88.5; DB 2; Length 289;			
Best Local Similarity 22.7%; Pred. No. 18;			
Matches 48; Conservative 18; Mismatches 60; Indels 85; Gaps 10;			
QY 20 SSTIVTGTCQSWSM-----IPWHQRTPEVNPAGLTMNYCRNPDSGKQPW 67			

Query Match Score 4.9%; Score 87.5; DB 2; Length 221;

Best Local Similarity 26.4%; Pred. No. 16;

Matches 29; Conservative 9; Mismatches 39; Indels 33; Gaps 4;

QY 193 YCNLITRCSDTEGYVAPPTVQVPSLGPSEQDMFGNGKSYRKATVYGTFCQEWAA 252

Db 72 YCGLT-----IQYPELNAQDILKPGF-----LITLGFPQNFGK 106

QY 253 QEPHRHSTFPIG---TINKWAGLEKNNYCRPFDGTDINGWYCYIMNPAPRLFDY 299

Db 107 QEPGDNELTLPGLKRYVPGKQFLPNEQLFAKGVDNGE----NEQRIFF 151

RESULT 9

JQ1209 attachment protein - human respiratory syncytial virus (strain RSB6614)

N;Alternate names: G protein syncytial virus

C;Species: human respiratory syncytial virus

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997

C;Accession: JQ1209

R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.

J. Gen. Virol. 72, 2091-2095, 1991

A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: JQ1204; MUID: 91374005; PMID: 1895054

A;Accession: JQ1209

A;Molecule type: mRNA

A;Residues: 1-297 <AN>

C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract

C;Superfamily: respiratory syncytial virus major surface glycoprotein G

C;Keywords: glycoprotein; transmembrane protein F; 85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 4.8%; Score 86.5; DB 2; Length 297;
Best Local Similarity 23.0%; Pred. No. 26;
Matches 57; Conservative 26; Mismatches 88; Indels 77; Gaps 13;

QY 66 PWCTTDPVCVRWEYCNIQCSPTESTEAVLETPTVPPVMSAEHSEAPTEQTPVYRCYHG 125
Db 88 PTYDQNQGIGISNL--SETTSOPATPAAL-TSAES----TQSTIVK--- 132

QY 126 NGQSTRGTFSTTYGTRICQSNSMTPHRHORTPENYPNGL---TMNYCRNPDADTGWC 182
Db 133 ----TQNTTIT--QIQQ-SKPTKQHONKPKNNHFEVNFYECSTCNSNNPTC 182

QY 183 F-----ITDPSRWEYCNUTRCSDTEGVAPPVYQVSLGPPSE 223
Db 183 WAICKRIPKKKKPKKKTPKTPKEVLT-----RPTE 232

QY 224 QDCMFNGNGKGYRGKAKT-VIGTPCQEWAAQEPHRHSTFPIGTTNKWAGLEKNVCRNPQGD 282
Db 233 KPTINTKNTNIRTLTNTTNTGPN--EYTSQKETLHSI-----SEGN 273

QY 283 INGPQCYT 290
Db 274 PSPSQVYT 281

RESULT 11
AB3130 transposase BMEL1424 [Imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hafius, S.; O'Callaghan, D.; Jetes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <KUR>
A;Cross references: GB:AE008817; PIDN:AAL52605.1; PID:g17983424; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics: BMEL1424
A;Map position: I

QY 30 QSNSSMTPHQRTPENYPNAGLT-----CRNPDSSKQPNWCYTIDPCY- 75
Db 10 QOVAVIAKP---LIFTNQFGAHTDRVISGITHILRSGCCRWQDC---PACYGPPRTVY 62

QY 76 -----YCNLTCQESTEAVLVEETPVYVPSKMEHSEA----- 111
Db 63 NRPHRM5AKGTWRRFEALVQFDTHMDSTA-----KAHRPAGGGDAEAIGR 116

QY 112 -----PHEQTPVYRCYHGNGQSYRGT-----FSTTV-----TGRT 142
Db 117 SRGRSRSKTHAVDSC--GRPVALKITPGQRGDAVILLDYSFQNVHSERIEETGVY 174

QY 143 CQWSMTPHQRTPENYPNGLT---MNYCRNPDADTG---FW---CFTTDS 188
Db 175 TPQFSRTPAPNEH---PQECPDTIASRNGGRSFRQAEGACTPLWGLAENCFSLLRT 231

QY 189 IR---WEYCNLRCSDTEGVAPPVYQVPSLGP-----PEQ 224
Db 232 VQDTWP-----GDDGSLVAPH--QPSNGPCHCRTDTPSSQ 267

RESULT 11
A85231 hypothetical protein AT4920350 [Imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
C;Accession: A85231
R;anonymous
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; PMID:20083488; PMID:10617198
A;Accession: A85231
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241 <STOP>
A;Cross-references: GB:NC_001268; PID:97268830; NID:97268830; PIDN:CA879035.1; GSPDB:GN00140
C;Genetics:
A;Map position: 4

Query Match 4.7%; Score 84.5; DB 2; Length 241;
Best Local Similarity 21.8%; Pred. No. 29;
Matches 42; Conservative 16; Mismatches 70; Indels 65; Gaps 9;

QY 95 TPTVVPYPSMEAHSAAEAPTQTPVYRCYHGNGQSYRGT-----TGRT 154
Db 11 TPTVYFINGF-----ITDEPQTQULNHTYAGSGSKW-----TIKRNRLQNGGMV-HEK 59

QY 155 QRTPENYP-----NDGLTMNYCRNPDADTGPNCFITDPSIRWEY 193
Db 60 GLVPQELPPWLTKITAEIHESGLFPSSAINHYLINE----- 104

QY 194 CNTPRCSDTEGTVVAPPVYQVPLGPESEQD---CMPNGNGKYYRGKXATVTPGPQC 249
Db 105 -----HODGPAYEF-----WVAILSLGSYVMDETPHLRURSGDGYISKDQ----SPCAE 150

QY 250 WAAQEPHHSHSTFI 262
Db 151 SCAPERDFSFSVLL 163

RESULT 12
T24703 hypothetical protein T08G3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T24703
R;Lloyd, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19926
A;Accession: T24703
A;Molecule type: DNA
A;Residues: 1-304 <WIL>
A;Cross-references: EMBL:283238; PIDN:CA805796.1; GSPDB:GN00023; CESP:T08G3.6
A;Experimental source: clone T08G3
C;Genetics:
A;Gene: CESP:T08G3.6
A;Map position: 5
A;Introns: 86/2

Query Match 4.7%; Score 84.5; DB 2; Length 304;
Best Local Similarity 19.1%; Pred. No. 37;
Matches 53; Conservative 33; Mismatches 108; Indels 83; Gaps 14;

QY 87 ETESGVLEPTVYVY-----PSMEAHSERAPTEQ-----VYROC 122
Db 26 EINFSEFKTRIVPLMSVQAGCGSYGAPRNALQNGPAKICTPGSSACROSLITYRV 85

QY 123 YHGNEQSYTGFTFTVY-----GRIC-----QSNWSMTPHQRHTPNN--YPNF 164
Db 86 --KGDTIRYILCNSKTCVTAQRTCCIFYVPMILINGSSQCGPPFKDPDRSSESPPCPKG 142

QY	165 GLTMN---YCRNPFDADGPW-----CFTIDPSIRWEYCNLIRCSDTEGYVAP 209	A;Experimental source: strain bristol N2; clone F49F1.1
Db	143 GFWSWSAYFR - DGEKAVSRTTRCLTEAGCPDGTIELSTAFCRLVDSL 200	C;Genetics:
A;Gene: CESP:F49F1.7		A;Map Position: 4
A;Introns: 42/2; 79/2; 116/2; 209/2		C;Species: Caenorhabditis elegans
QY	210 PTVIQVPSLGLPP - SEODCMFGNGKGYRGKKATTGTCOEWAQEPHRHSTEI----PG 264	C;Superramain: Caenorhabditis elegans hypothetical protein F49F1.6
Db	201 XTNGLTYTINPYNDNECTASQVN----ESQKSAVEPCNEYTSWKYTRWTAHYVKPG 256	
QY	265 TNKAGLLEKNYCNPQDINGPWTMMPRKEDIDCD 301	Query Match 4.6%; Score 82; DB 2; Length 240;
Db	257 RSDTVGIKTSNOE-----AAHEKTKFLYCD 281	Best Local Similarity 21.1%; Pred. No. 44; Mismatches 74; Gaps 9;
RESULT 13		Matches 44; Conservative 17; Mismatches 74; Gaps 9;
JQ1208	attachment protein - human respiratory syncytial virus (strain RSB6256)	QY 28 TQCSWSSMIPHWHORT----PENYNAGLTENYCRNPQCYTDPVCYRWEYCNL 82
A;Alternate name: G protein	C;Species: human respiratory syncytial virus	Db 57 TCSDTNSDCKEFHCMVMPYEQCKS-----CGICDSAPTWMD ---HWPECPK 105
C;Species: human respiratory syncytial virus	C;Accession: JQ1208	83 TQ---CGETE-----SGVLTPTIVVPVSMAEHSEAPPEQT 116
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997		Db 106 YQYPCESETERIKCPRSCDAGCNPSTIKEASVTTINGHLDIGTRRLQATQTKSPETTIT 165
P;Canee, P.A.; Matthews, D.A.; Pringle, C.R.		QY 117 PVYRCYHGNGQSYFRGTFSTTIVGRICQSMSSMTPHRQRTPENYNDGLTMAYCRNPD 176
J. Gen. Virol. 72, 2091-2096, 1991		Db 166 ETK-----AKTTTETTAKTTTIPSTVKTYYKPE-----KPECT 204
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A		QY 177 DRGPWC-----FTTD----PSIRWEYC 194
A;Reference number: JQ1204; PMID:91374005; PMID:1095054		Db 205 DSSPNCTTWAKNGFCTNTFPPEKRKEYC 233
A;Accession: JQ1208		
A;Molecule type: mRNA		
A;Residues: 1-297 <CAN>		
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract illness and adults.		RESULT 15
C;Superfamily: respiratory syncytial virus major surface glycoprotein G		T19913
C;Keywords: glycoprotein; transmembrane protein		hypothetical protein C43F9.5 - Caenorhabditis elegans
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict		C;Species: Caenorhabditis elegans
Query Match 4.7%; Score 83.5; DB 2; Length 297;		C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Best Local Similarity 22.6%; Pred. No. 43;		C;Accession: T19913
Matches 56; Conservative 26; Mismatches 89; Indels 77; Gaps 13;		C;Submitted to the EMBL Data Library, November 1996
QY 66 PWCTTDPCEPVRWEYCNLUTQCSSETEGVLIETPTVPPVSMEAHSRAAPTHQTPVYRQCYH 125		A;Reference number: Z11915
Db 88 PTYLQNPLGLIFSNL--SETTS---QPTTPATTPS--AESIPQSTIVK-----132		A;Status: preliminary; translated from GB/EMBL/DBJ
QY 126 NGQSYRGTGSTTYGRTCQSWSMTPHRHRTPEYNTNDGL----TMNYCRNPDAUTGPWC 182		A;Molecule type: DNA
Db 133 -----TKNTT-----QIQP-SKPTKQRQNKPKNNDHFEEVNFVPCSTCSNNPTC 182		A;Residues: 1-248 <WIL>
QY 183 F-----TIDPCEPVRWEYCNLUTQCSSETEGVLIETPTVPPVSMEAHSRAAPTHQTPVYRQCYH 223		A;Cross-references: EMBL:Z82262; PIDN:CAF05152.1; GSPDB:GN000022; CESP:C43F9.5
Db 183 WAICKRIPKKPKKTTKPKKPK-----TIDKLKQTTKPKKEYLT----KPTE 232		A;Experimental source: clone C43F9
QY 224 QDCMFNGKGYRKKAT - VIGTPQEWAAQEPHRHSTPIFGTNKWAGLEKNYCRNEDGD 282		A;Genetics:
Db 233 KPTINTTRNIRNLTTNTTGNP - EYTSQKETLHST-----SEGN 273		A;Map Position: 4
QY 283 INGPQYI 290		A;Introns: 4/1; 78/3; 118/1; 193/3
Db 274 PSPSQYT 281		
RESULT 14		
T33698	hypothetical protein F49F1.7 - Caenorhabditis elegans	QY 13 GRSYRGISS---TIVYGRTCQSWSMTPHRHRTPEYNTNDGL-----TIVYGRTCQSWSMTPHRHRTPEYNTNDGL 67
C;Species: Caenorhabditis elegans		Db 20 GLTTELGRSKRQTHCGRPNQFYSMPCYWTSSQTRN-----PYTCANGGRKGIGVG 72
C;Accession: T33698		QY 68 CYTTDPCEPVRW --EXCNAJQCSETESEVLEIETPTVPPVSMEAHSRAAPTHQTPVYRQCYH 124
R;Miller, N.; Wamsley, P.		Db 73 CYTNYQQTPTYANSVY-LANCCOTNPVVTTRAPIPTT-----TTSVSYALAYCN 122
submitted to the EMBL Data Library, October 1998		QY 125 GNQSYRGTGSTY-TVYGRTCQSWSMTPHRHRTPEYNTNDGL-----TIVYGRTCQSWSMTPHRHRTPEYNTNDGL 180
A;Description: The sequence of C. elegans cosmid F49F1.		Db 123 GQHQVQCTSVDCAGQTCMNGICCT-----TGTNETTGSCGGLDAISAO----GTCQ 172
A;Accession: T33698		QY 181 WC---FTTDPSIRWEYCNLUTRCSDEGTVAPPVYQVPSLGPSEQDCMFNGKGYRKK 238
A;Status: preliminary; translated from GB/EMBL/DBJ		Db 173 TCGSFRCSTS---NYCCEQYQGRTAG-----LCNGCPTGTSNSNTGNGY--CC 217
A;Residues: 1-240 <WIL>		QY 239 ATVTPGP 246
A;Cross-references: EMBL:AFF00656; PIDN: AAC68946.1; GSPDB:GN00022; CESP:F49F1.7		Db 218 ATCAGRP 225

Wed Oct 1 15:58:32 2003

us-10-088-548-2.sep29.rpr

Page 6

Search completed: September 29, 2003, 08:04:08
Job time : 23 secs

A protein - protein search, using sw model						
Copyright (c) 1993 - 2003 Compugen Ltd.						
Run on: September 29, 2003, 08:01:08 ; Search time 11 Seconds (without alignments) 1316.748 Million cell updates/sec						
title: US-10-088-548-2	sequence: 1 KSPVVDQYHGDGRSYRGIS.....YTMMNPKLFYCDIPLCASS 308	scoring table: BLOSUM62	Gapop 10.0 , Gapext 0.5	searched: 127863 seqs, 47026705 residues	total number of hits satisfying chosen parameters: 65706	post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries
database : Swissprot_41:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES				
result No.	Score	Query Match Length	DB ID	Description	%	Query
1	620	34.7	169	1 PLMN_RAT	001177 rattus norvegicus	WVGIG_HRSV1
2	88.5	5.0	277	1 SNN4_HUMAN	P42489 homo sapiens	WVGIG_HRSV1
3	86.5	4.8	297	1 VGIG_HRSV1	P21655 mus musculus	VGIG_HRSV1
4	84.5	4.7	221	1 GSHE_MOUSE	P21655 mus musculus	VGIG_HRSV1
5	83	4.7	297	1 GSHE_MOUSE	P20205 human resp	VGIG_HRSV1
6	77.5	4.4	221	1 GSHE_RAT	P30710 rattus norvegicus	VGIG_HRSV1
7	77	4.3	221	1 GSHE_MACPA	P28714 macaca fasciata	VGIG_HRSV1
8	75	4.2	292	1 VGIG_HRSV1	P23414 human resp	VGIG_HRSV1
9	75	4.2	127	1 VAP_BABIT	P09412 oryctoidea lagomys	VGIG_HRSV1
10	75	4.2	221	1 GSII_RAT	Q66625 ratus norvegicus	VGIG_HRSV1
11	74.5	4.2	219	1 GSHE_PIG	Q18994 sus scrofa	VGIG_HRSV1
12	74	4.1	224	1 PWP4_XENLA	P00223 xenopus laevis	VGIG_HRSV1
13	74	4.1	271	1 IOLB_BACSU	P42413 bacillus	VGIG_HRSV1
14	73.5	4.1	292	1 VGIG_HRSV1	P20596 human resp	VGIG_HRSV1
15	73	4.1	265	1 KNHL_CANGA	Q76584 candida gillettei	VGIG_HRSV1
16	73	4.1	300	1 PEG6_HUMAN	Q95407 homo sapiens	VGIG_HRSV1
17	72.5	4.1	217	1 SGS3_DROS1	P13729 drosophila	VGIG_HRSV1
18	72.5	4.1	221	1 GSHE_HUMAN	Q77151 homo sapiens	VGIG_HRSV1
19	72.5	4.1	269	1 NEP1_HUMAN	Q95927 homo sapiens	VGIG_HRSV1
20	72	4.0	263	1 SGS3_DROTA	P13728 drosophila	VGIG_HRSV1
21	72	4.0	272	1 TWR4_MOUSE	P47741 mus musculus	VGIG_HRSV1
22	72	4.0	297	1 VGIG_HRSV1	P27023 human resp	VGIG_HRSV1
23	71.5	4.0	162	1 HX9_CAVFO	P15783 canis familiaris	VGIG_HRSV1
24	71.5	4.0	221	1 GSHE_CANFO	Q46607 canis familiaris	VGIG_HRSV1
25	71	4.0	226	1 GSHD_HUMAN	P22352 homo sapiens	VGIG_HRSV1
26	71	4.0	227	1 CNG5_HUMAN	Q98110 homo sapiens	VGIG_HRSV1
27	71	4.0	308	1 HMBL_STROP	P15545 strongylidae	VGIG_HRSV1
28	70.5	3.9	169	1 GPO_SINY3	P71250 synechocystis	VGIG_HRSV1
29	70.5	3.9	261	1 Y612_SINY3	P72381 synechocystis	VGIG_HRSV1
30	70	3.9	241	1 WAP8_HUMAN	Q8ua00 homo sapiens	VGIG_HRSV1
31	69.5	3.9	283	1 HX9_FUGRU	Q42506 fugu rubripinnis	VGIG_HRSV1
32	69.5	3.9	307	1 HMBL_TRIGGER	P09080 trinectes	VGIG_HRSV1
33	69	3.9	199	1 FEST_TIGER	P8A139 actinia equina	VGIG_HRSV1

DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.	FT SIGNAL 1 21 POTENTIAL, SECRETORY GLUTATHIONE
KW Oxidoreductase; Peroxidase; Signal.	FT EPIDIDYMAL SECRETORY GLUTATHIONE
FT SIGNAL 1 21	FT PEROXIDASE.
FT CHAIN 22	FT BY SIMILARITY.
FT ACT_SITE 73	FT 32AA912ED6C73D93 CRC64;
FT SEQENCE 221 AA; 25384 MW;	FT BY SIMILARITY.
Query Match Score 79; DB 1; Length 221;	FT Best Local Similarity 26; Conservative 11; Mismatches 40; Pred. No. 20; Gaps 4;
Best Local Similarity 25.0%; Pred. No. 15;	FT Matches 26; Conservative 11; Mismatches 40; Pred. No. 20; Gaps 4;
Matches 24; Conservative 9; Mismatches 35; Indels 28; Gaps 3;	FT Query Match Score 77.5; DB 1; Length 221;
QY 193 YCNLTCRCSDEGTYVAPPVQYPSLGPPESEQDCMFGNGKGYRKAKATVTPCQEWAA 252	FT Best Local Similarity 26; Conservative 11; Mismatches 40; Pred. No. 20; Gaps 4;
Db 72 YCGLT-----IYYPEINALDDDLRQFG-----IVILGFPNCNDFGK 106	FT Matches 26; Conservative 11; Mismatches 40; Pred. No. 20; Gaps 4;
QY 253 QEPHRHSTFIPG---TNKWAGLEKKNYCRNPDGIDNG 285	FT Query Match Score 73.6; DB 1; Length 221;
Db 107 QSEGDNTEIILPGLKLYVRPGKGFLPQLFAKGVDNG 142	FT Best Local Similarity 26; Conservative 11; Mismatches 40; Pred. No. 20; Gaps 4;
RESULT 8	
VGLG_HRSV8 STANDARD; PRT; 292 AA.	
TD VGLG_HRSV8	TD P23041; AC P23041; DT 01-NOV-1991 (Rel. 20, Created)
AC GSHE_MACFA	DT 01-NOV-1991 (Rel. 20, Last sequence update)
AC P28114;	DT 01-JUL-1992 (Rel. 23, Last annotation update)
AC GSHE_MACFA	DE Major surface glycoprotein G (Attachment glycoprotein G).
AC P28114;	GN Human respiratory syncytial virus (subgroup B / strain 8/60).
AC P28114;	OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
AC P28114;	OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
AC P28114;	OC NCBI_TaxID=11255;
AC P28114;	OX RN [1].
AC P28114;	RP SEQUENCE FROM N.A.
AC P28114;	RX MEDLINE-90357765; PubMed=1697126;
AC P28114;	RA Sullender W.M., Anderson K., Wertz G.W.;
AC P28114;	RT "The respiratory syncytial virus subgroup B attachment glycoprotein:
AC P28114;	RT analysis of sequence, expression from a recombinant vector, and heterologous
AC P28114;	RT subgroup virus challenge." R
AC P28114;	RT Sullender W.M., Muison M.M., Anderson L.J., Wertz G.W.;
AC P28114;	RN [2].
AC P28114;	RP SEQUENCE FROM N.A.
AC P28114;	RX MEDLINE-91314593; PubMed=1895391;
AC P28114;	RA Sullender W.M., Muison M.M., Anderson L.J., Wertz G.W.;
AC P28114;	RT "Genetic diversity of the attachment protein of subgroup B
AC P28114;	RT respiratory syncytial viruses." R
AC P28114;	RL J. Virol. 65:545-534 (1991).
AC P28114;	CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
AC P28114;	CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
AC P28114;	CC REAGGREGATING ACTIVITIES.
AC P28114;	CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
AC P28114;	CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
AC P28114;	CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
AC P28114;	CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
AC P28114;	CC
AC P28114;	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
AC P28114;	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
AC P28114;	CC the European Bioinformatics Institute. There are no restrictions on its
AC P28114;	CC use by non-profit institutions as long as its content is in no way
AC P28114;	CC modified and thus statement is not removed. Usage by and for commercial
AC P28114;	CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
AC P28114;	CC or send an email to license@isb-sib.ch).
AC P28114;	CC
AC P28114;	CC DR EMBL; NS5633; AAA47413.1; -.
AC P28114;	DR PIR; S24327; S24327.
AC P28114;	DR HSSP; P00435; ISP1.
AC P28114;	DR InterPro; IPR00889; Glut_peroxidase.
AC P28114;	DR Pfam; PF0025; GSHP2; 1.
AC P28114;	DR PRINTS; PRO011; GlutPeroxidase.
AC P28114;	DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
AC P28114;	DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
AC P28114;	KW Oxidoreductase; Peroxidase; Signal.
DR X62403; CAA44273.1; -.	DR CYTOPLASMIC (POTENTIAL).
DR PIR; S24327; S24327.	DR PIR; A37077; MGNE60.
DR HSSP; P00435; ISP1.	DR InterPro; IPR006925; Glycoprot_G.
DR InterPro; IPR00889; Glut_peroxidase.	DR Pfam; PF00802; Glycoprotein_G; 1.
DR Pfam; PF0025; GSHP2; 1.	KW Transmembrane, Glycoprotein.
DR PRINTS; PRO011; GlutPeroxidase.	FT DOMAIN 1 37
DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.	FT TRANSMEM 38 66
DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.	FT DOMAIN 67 292
KW Oxidoreductase; Peroxidase; Signal.	POTENTIAL, EXTRACELLULAR (POTENTIAL).

FT	CHAIN	22	219	EPIDIDYMAL SECRETORY GLUTATHIONE PEROXIDASE.
FT	ACT_SITE	73	73	BY SIMILARITY.
SQ	SEQUENCE	221 AA;	24961 MW;	92749IAF6A3EF8C CRC64;
Query Match Score: 75; DB: 1; Length: 221;				
Best Local Similarity: 25.0%; Pred. No.: 31;				
Matches: 23; Conservative: 13; Mismatches: 32; Gaps: 3;				
Indels: 24; Gaps: 3; Gaps: 4;				
QY 227 MFGNGKGRKGKAT-----MTVTPGQWAAQPHHRHSTIPG---TWR 267	Query Match Score: 4.2%; Score: 74.5%; DB: 1; Length: 219;			
DB 65 LFVNIVASFCGLIATYPANTLQEELRPPNVSYLGPFCNQFGKQEDGHNSEILLGKVKYVRP 124	Best Local Similarity: 24.5%; Pred. No.: 34;			
QY 268 WAGLEKNTCRNPDPDINGPACYTNPRKLFDY 299	Matches: 27; Conservative: 10; Mismatches: 40; Indels: 33; Gaps: 4;			
DB 125 GGGFVPNFOLFERGVDYGD----NEQRVFSF 151	Query Match Score: 4.2%; Score: 74.5%; DB: 1; Length: 219;			
QY 253 QEPHRHSTPIPG---TINKWAGLEKNYCNPDDINGPACYTMNPRKLFDY 299	Best Local Similarity: 24.5%; Pred. No.: 34;			
DB 105 QEPGENSETILGLKVKYVRGGGYVPNFQLFEKGVNCE----KEQQVETF 149	Matches: 27; Conservative: 10; Mismatches: 40; Indels: 33; Gaps: 4;			
RESULT 11				
GSFP_PIG	ID	GSH_E_PIG	STANDARD;	PRT;
AC	ID	Q88994;	STANDARD;	PRT;
DT	ID	AP4_XENNA	STANDARD;	PRT;
DT	ID	Q00222;	STANDARD;	PRT;
DT	ID	Q04155;	STANDARD;	PRT;
DT	ID	Q04213;	STANDARD;	PRT;
DE	Created)	01-OCT-1994 (Rel. 30, Last sequence update)		
DE	Created)	01-OCT-1994 (Rel. 30, Last annotation update)		
DE	Epoxidymal secretory glutathione peroxidase precursor (EC 1.11.1.9)	15-SEP-2003 (Rel. 42, Last annotation update)		
(Bp)Epoxidymal-specific glutathione peroxidase-like protein (EC1P).				
GN	"xP1 and xP4. P-domain peptides expressed in Xenopus laevis precursor.			
GN	XFX5.			
OS	Xenopus laevis (African clawed frog)			
OS	Sus scrofa (Pig)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBITaxonID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 22-46.			
RC	TISSUE=Epoxidymis;			
RX	MMDBLINE=9145156; PubMed=9271255;			
RA	Ohamura N., Iwaki Y., Hiramoto S., Tamba M., Banai S., Sugita Y.,			
RA	Santini P., Dacheux F., Dacheux J. L.;			
RT	Molecular cloning and characterization of the epoxidymis-specific			
RT	glutathione peroxidase-like protein secreted in the porcine			
RT	epoxidymal fluid.";			
RL	Biochim. Biophys. Acta 1336:99-109 (1997).			
CC	- FUNCTION: MAY CONSTITUTE A GLUTATHIONINE PEROXIDASE-LIKE PROTECTIVE SYSTEM AGAINST PEROXIDE DAMAGE IN SPERM MEMBRANE.			
CC	LIPIDS. SINCE THE PURIFIED PORCINE ENZYME HAS VERY LITTLE ACTIVITY TOWARDS HYDROGEN PEROXIDE OR ORGANIC HYDROPEROXIDES THE PROTECTIVE EFFECT IS NOT LIKELY TO BE EXERTED BY ITS ENZYMATIC ACTIVITY. INSTEAD, MAY PROTECT SPERM FROM PREMATURE ACROSOME REACTION IN THE EPIDIDYMIS BY BINDING TO LIPID PEROXIDES, WHICH MIGHT OTHERWISE INTERACT WITH PHOSPHOLIPASE A2 AND INDUCE THE ACROSOME REACTION.			
CC	-4 CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + 2 H(2)O.			
CC	- CC SUBUNIT: Homotetramer.			
CC	-1 SUBCELLULAR LOCATION: Proximal caput epoxidymis.			
CC	-1 TISSUE SPECIFICITY: Belongs to the glutathione peroxidase family.			
CC	-1 SIMILARITY: Belongs to the glutathione peroxidase family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; M75034; BAA0003.1; -			
DR	PIR; B40850; B40850.			
DR	HSSP; P04155; IPI52.			
DR	InterPro; IPR00519; P_trefoil.			
DR	SMART; SM00018; trefoil; 4.			
DR	PROSITE; PS00025; P_TREFOIL; 4.			
DR	KW Signal; Growth factor; Glycoprotein; Repeat.			
FT	SIGNAL 1 17 POTENTIAL.			
FT	CHAIN 18 224 POTENTIAL.			
FT	FT DOMAIN 26 67 POTENTIAL.			
FT	FT DOMAIN 74 116 POTENTIAL.			
FT	FT DOMAIN 124 166 POTENTIAL.			
FT	FT DOMAIN 174 215 POTENTIAL.			
FT	DISULFID 27 53 BY SIMILARITY.			
FT	DISULFID 37 52 BY SIMILARITY.			
FT	DISULFID 47 64 BY SIMILARITY.			
FT	DISULFID 75 102 BY SIMILARITY.			
FT	DISULFID 86 149 BY SIMILARITY.			

FT	DISULFID	96	113	BY SIMILARITY.		Sotokin A., Taconi E., Takagi T., Takahashi H., Takenaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpatra P., Toononi A., Tosato V., Uchiyama S., Vandebilt M., Vannier F., Vassarotti A., Viatr A., Wambutt R., Wedler E., Weitzsaegeger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yoshida K., Yoshihikawa H.F., Zumstein E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> ."
FT	DISULFID	125	152	BY SIMILARITY.		RT
FT	DISULFID	136	163	BY SIMILARITY.		RT
FT	DISULFID	146	201	BY SIMILARITY.		RA
FT	DISULFID	175	200	BY SIMILARITY.		RA
FT	DISULFID	185	212	BY SIMILARITY.		RA
FT	DISULFID	195	212	BY SIMILARITY.		RA
FT	CARBONOID	104	104	N-LINED (GLCNAC; . . .) (POTENTIAL).		RT
SQ	SEQUENCE	224 AA;	24815 MW;	6AE0SB3429EPC635 CR64;		RL
Query Match		4.18;	Score 74;	DB 1;	Length 224;	RN [3]
Best Local Similarity	22.28;	Prcd. No. 38;				RP SEQUENCE OF 1-71 FROM N.A.
Matches	38;	Conservative 25;	Minmatches 70;	Indels 38;	Gaps 10;	RA STRAIN=168 / BGSC1A1;
QY	42	RPTENYNAGTENTC-----RNPDSGKQPWCYTDPPVRYXCNITQCSETEGV 92				RC MEDLINE=96053926; PubMed=7584049;
Db	32	KSNRNCGGPGLSPDCCVKKGCCFDSDPDS--IWCYIP---WKFED-TICNPAAEKA 82				RA Yoshiba K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;
QY	93	LETPPTVVPVMEALSEAAPTEP-PVYRCOYHNGNSQRGTFSTVTGFTCQWSMTP 151				RA "Cloning and sequencing of a 36-kb region of the <i>Bacillus subtilis</i> genome between the gnt and iol operons."
Db	83	RVNCGYGPITISQDCDKKGOCNPDITVPPVYKQYRPIEVE-----RDC---SAVEP 130				RA RT I- PATHWAY: Myo-inositol catabolism.
QY	152	HRRHQ---TPENYPNGLMTNYCRNPDAADTGWPCTTDPSIRWYCNTRGS 200				CC This SWISS-PROT entry is copyright. It is produced by a collaboration between the Swiss Institute of Bioinformatics and the EMBL, our station -
Db	131	KKRVVNGGPGVSPDDCIKNGCCPNSDVGWPWCF--KPEIKKE--LLQCA 176				CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RESULT 13						CC
ID	IOLB_BACSU	STANDARD;	PRT;	271 AA.		CC DR EMBL: D14399; BAA03291.1; -
AC	P42413;					CC DR EMBL: D29124; CAB1601.1; -
DT	01-NOV-1995	(Rel. 32, Created)				CC DR EMBL: AB005524; BAA1610.1; -
DT	01-NOV-1995	(Rel. 32, Last sequence update)				CC DR PIR: B664645.
DE	28-FEB-2003	(Rel. 41, Last annotation update)				CC DR SubList: BG1118; iolB.
GN	IOLB OR B83B					KW Complete Proteome.
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i>					SQ SEQUENCE 271 AA; 30770 MW; 43224E4C18DF21F3 CRC64;
DB	NCBI_TaxID=123;					Query Match 4.1%; Score 74; DB 1; Length 271;
RN	SEQUENCE FROM N.A.					Best Local Similarity 20.3%; Pred. No. 47;
RC	STRAIN=168 / BGSC1A1;					Matches 42; Conservative 19; Mismatches 64; Indels 82; Gaps 10;
RX	MEDLINE=9503891; PubMed=7952181;					QY 101 VPNEAEEAATPTEOTP-----VROCY-----HNGQSYR 131
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					DR 76 IGPRESFERAPTDWSVYNDRAFEITAVSDARYALCYSPEKQLPTKLIAEDNGIEHR 135
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					QY 132 GTFSTTYTGRT-----CQSWSSMTPHRQHQTPEPNYNDG-LTMAY 170
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	DR 136 GQSNKTRVHNLLPSDPAANSLLVVYDGSWTSPPPHKDQ-DNPFEEFLETFY 193				
RN	SEQUENCE FROM N.A.					QY 171 CRNPDAATG---PWDFTTDPSIRNEYCNLTCSDTEGTVAATTQPS---LGPPSE 223
RC	MEDLINE=98044033; PubMed=9384377;					DB 194 YHELDPGQQGFYQRTYDORSI-----DETMVGNENVTVTPAGYHPVGVD- 240
RX	RUNST F., Ogasawara N., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	QY 224 QDCMFNGKGRGKAKATGTCQEW 250				
RA	Human respiratory syncytial virus (subgroup B / strain 18537).					DB 241 -----GTTSYLNWAG-PTRKW 257
RA	Virus: SSRNA negative-strand viruses; Mononegavirales; Paranyxoviridae; Pneumovirinae; Pneumovirus.					RESULT 14
RA	NCBI_TaxID=1251;					VIGL_HRSV1 STANDARD; PRT; 292 AA.
RA	SEQUENCE FROM N.A.					AC P20816; PRT; 292 AA.
RA	STRAIN=168 / BGSC1A1;					DT 01-FEB-1991 (Rel. 17, Created)
RA	MEDLINE=9503891; PubMed=7952181;					DT 01-FEB-1991 (Rel. 17, Last sequence update)
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					DT 01-NOV-1991 (Rel. 20, Last annotation update)
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					DE Major surface glycoprotein G (Attachment glycoprotein G).
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	AC P20816; PRT; 292 AA.				
RA	Human respiratory syncytial virus (subgroup B / strain 18537).					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Virus: SSRNA negative-strand viruses; Mononegavirales; Paranyxoviridae; Pneumovirinae; Pneumovirus.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	NCBI_TaxID=1251;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	SEQUENCE FROM N.A.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	MEDLINE=9503891; PubMed=7952181;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	AC P20816; PRT; 292 AA.				
RA	Human respiratory syncytial virus (subgroup B / strain 18537).					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Virus: SSRNA negative-strand viruses; Mononegavirales; Paranyxoviridae; Pneumovirinae; Pneumovirus.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	NCBI_TaxID=1251;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	SEQUENCE FROM N.A.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	MEDLINE=9503891; PubMed=7952181;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	AC P20816; PRT; 292 AA.				
RA	Human respiratory syncytial virus (subgroup B / strain 18537).					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Virus: SSRNA negative-strand viruses; Mononegavirales; Paranyxoviridae; Pneumovirinae; Pneumovirus.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	NCBI_TaxID=1251;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	SEQUENCE FROM N.A.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	MEDLINE=9503891; PubMed=7952181;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	AC P20816; PRT; 292 AA.				
RA	Human respiratory syncytial virus (subgroup B / strain 18537).					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Virus: SSRNA negative-strand viruses; Mononegavirales; Paranyxoviridae; Pneumovirinae; Pneumovirus.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	NCBI_TaxID=1251;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	SEQUENCE FROM N.A.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	MEDLINE=9503891; PubMed=7952181;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	AC P20816; PRT; 292 AA.				
RA	Human respiratory syncytial virus (subgroup B / strain 18537).					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Virus: SSRNA negative-strand viruses; Mononegavirales; Paranyxoviridae; Pneumovirinae; Pneumovirus.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	NCBI_TaxID=1251;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	SEQUENCE FROM N.A.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	MEDLINE=9503891; PubMed=7952181;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D., Porwollik S., Prescott A.M., Presecan E., Pujić P., Purcell C., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rose M., Sadie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scorfone F., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,	AC P20816; PRT; 292 AA.				
RA	Human respiratory syncytial virus (subgroup B / strain 18537).					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Virus: SSRNA negative-strand viruses; Mononegavirales; Paranyxoviridae; Pneumovirinae; Pneumovirus.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	NCBI_TaxID=1251;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	SEQUENCE FROM N.A.					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	MEDLINE=9503891; PubMed=7952181;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	"Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon."					RA Human respiratory syncytial virus (subgroup B / strain 18537).
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., Errington K.D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Galuzzi A., Lardinois S., Galloren N., Kondo F., Moszer I., Albertini A.M., Allord G., Borchert S., Boursier L., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capon V., Carter N.M., Chai S.M., Guy B.J., Haga K., Haiech J., Harwood C.R., Hennaut A., Hilbert H., Holsappel S., Bosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamoto D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koerter P., Koenigstein G., Krieg S., Kumano M., Kurita K., Lepidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Neone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Porteille D					

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:01:08 ; Search time 36 Seconds
 (without alignments)
 2207.783 Million cell updates/sec

Perfect score: 1786

Sequence: 1 KSPVYQDCYHGDRSYRQIS.....YMMPRKLFYCDIDPLCLASS 308

Scoring table: BLOSUM62

Gapext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters: 513101

Minimum DB seq length: 0

Maximum DB seq length: 308

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_arachnid:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_hexapod:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_nic:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rhodobiont:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

17	243.5	13.6	211	11	055027	mus musculu
18	241	13.5	60	4	Q9UKJ7	homo sapien
19	231.5	13.0	90	4	Q8NG20	
20	225	12.6	202	13	Q96675	gallus gallu
21	210.5	11.8	75	6	Q9BGN9	openg bos tauru
22	168	9.4	111	6	Q77688	oryctolagus
23	165.5	9.3	157	6	Q9rva8	bos tauru
24	159	8.9	231	11	Q8C6L2	Q96612 mus musculu
25	152	8.5	154	4	Q96SE8	homo sapien
26	141	7.9	25	4	Q9UD88	homo sapien
27	117	6.6	263	4	Q90318	homo sapien
28	117	6.6	263	4	Q96EE7	homo sapien
29	117	6.6	263	4	QBNCT9	homo sapien
30	114	6.4	162	11	Q8C4E2	Q844e2 mus musculu
31	114	6.4	286	4	Q13209	homo sapien
32	95.5	5.3	214	6	Q9XT70	Q9x70 cryctolagus
33	91	5.1	261	5	Q9rav5	Q9rav5 drosophilu
34	90.5	5.1	268	10	Q42830	Q42830 phytopthor
35	89.5	5.0	289	16	Q8ZJU7	Q8zju7 salmonella
36	88.5	5.0	289	16	Q8ZCT3	Q8zct3 salmonella
37	87.5	4.9	223	4	Q36RT0	Q36rt0 medicago tr
38	87	4.9	249	10	Q24102	Q96bh3 homo sapien
39	86.5	4.8	223	4	Q96BH3	Q96bh3 homo sapien
40	86.5	4.8	295	12	Q86361	Q86361 respiratory
41	85.5	4.8	272	16	Q8YF06	Q8yf06 brucella me
42	85	4.8	234	11	Q9CU03	Q9cuj3 mus musculu
43	84.5	4.7	220	4	Q9H4C8	Q9hc8 homo sapien
44	84.5	4.7	221	11	Q8CD05	Q8cdq5 mus musculu
45	84.5	4.7	241	10	Q9SUP1	Q9sup1 arabidopsis

ALIGNMENTS

RESULT 1

Q9UR5	Q9UR5	PRELIMINARY;	PRT;	113 AA.
ID	Q9UR5;			
AC	Q9UR5;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TRIMBREL 23, Last annotation update)			
DE	ApolipoproteinA (Fragment)			
GN	APOA			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TAXID:9606;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	%
1	644	36.1	113	4	Q9UR5		Q9UR5 homo sapien	
2	634	35.5	113	4	Q9UR5		Q9UR5 homo sapien	
3	550.5	30.8	215	13	Q9UR5		Q9UR5 homo sapien	
4	544	30.5	95	4	Q8N696		Q8N696 homo sapien	
5	498	27.9	132	4	Q16609		Q16609 homo sapien	
6	489	27.4	113	4	Q9UR5		Q9UR5 homo sapien	
7	481.5	27.0	290	4	Q02935		Q02935 homo sapien	
8	477.5	26.7	296	4	Q14519		Q14519 homo sapien	
9	467.5	26.2	145	6	Q28911		Q28911 macaca fasci	
10	466	26.1	132	4	Q8TC02		Q8TC02 homo sapien	
11	445	24.9	105	4	Q9UR5		Q9UR5 homo sapien	
12	261.5	14.6	109	6	Q91LB8		Q91LB8 ovis aries	
13	260	14.6	209	11	Q8517		Q8517 mus musculu	
14	249.5	14.0	208	4	Q9YMO0		Q9YMO0 homo sapien	
15	249.5	14.0	210	4	Q13494		Q13494 homo sapien	
16	248	13.9	53	4	Q9D112		Q9D112 homo sapien	

SEQUENCE FROM N.A.
 RX MEDLINE:21181705; PubMed=11285247;
 RA Ogoelkova M., Kraft H.G., Entholm C., Uttermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) Kringle IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";
 CC "-1 SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; API158662; AA03680.1; JOINED.
 RL Hum. Mol. Genet. 10:815-824 (2001).
 DR HSSP; P00747; IPIK.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; kringle_1.
 DR PRINTS; PR000018; KRINGLE.
 DR ProDom; PD000395; Kringle_1.
 DR SMART; SM00130; kringle_1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50000; KRINGLE_2; 1.
 KW Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 ET NON_TER 113
 SQ SEQUENCE 113 AA; 1285 MW; F3D5681D9BS253A CR064;
 Query Match 36.1%; Score 644; DB 4; Length 113;
 Best Local Similarity 99.18%; Pred. No. 1.2e-49;

SQ	SEQUENCE	145 AA;	16097 MW;	0D2DA20A06A5DD87 CRC64;	RESULT 11
Query Match	Score 467.5; DB 6; Length 145;				Q9UTR8 PRELIMINARY; PRT; 105 AA.
Best Local Similarity	64.7%; Pred. No. 7e-34;				ID Q9UTR8 ID Q9UTR8;
Matches	86; Conservative 11; Mismatches 25; Indels 11; Gaps 2;				AC Q9UTR8;
QY	102 PSMEASE-----AAPLEQTIVVRCYHGNGSYRGTTESTVGRTCOSWSSMTP 151				DT 01-MAY-2000 (TRIMBUREL 13, Created)
Db	14 PTE-EKEVLLFLKSAPEQSIVQLCYHGDDGSYOQSSTTIVTERTCQAWSEMEP 72				DT 01-MAR-2003 (TRIMBUREL 15, Last sequence update)
Qy	152 HREHQRPENVPNGDITMCRNPAADTGPCQFTDPSRVEWCNLTCSDFTEGVAPPT 211				DT 01-MAR-2003 (TRIMBUREL 23, Last annotation update)
Db	73 HQHNRTEETNPAGNSIRKNCRAPDPVAAPICYTMDDPNVREWCNLTCSDAESTAVAPPN 132				DE Apolipoprotein(a) (Fragment).
QY	212 VIVQPSGQPPPEQ 224				GN Homo sapiens (Human).
Db	133 VVLYPSLEAFSEQ 145				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606;
SEQUENCE FROM N.A.					OC
RP					RN [1]
RX					SEQUENCE FROM N.A.
RX					MEDLINE:21181705; PubMed=11285247;
RX					RJ Ogorzalkova M., Kraft H.G., Ehnholm C., Uttermann G.; "Single nucleotide polymorphisms in exons of the apo(a) Kringle IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians." J. Hum. Mol. Genet. 10:1915-8(2001).
DR					-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR					CC AF156556; AAP03677.1;
DR					EMBL: AF156556; AAP03677.1;
DR					EMBL: AF156555; AAP03677.1; JOINED.
DR					HSSP; P00747; 2PK4.
DR					InterPro: IPR000001; Kringle.
DR					Pfam: PF00051; Kringle_1.
DR					PRINTS: PRO0018; KRINGLE.
DR					ProDom: PD00039; Kringle_1.
DR					SMART: SM00130; KR_1.
DR					PROSITE: PS00021; KRINGLE_1; 1.
DR					PROSITE: PS00070; KRINGLE_2; 1.
DR					Glycoprotein; Kringle; Lipoprotein.
KW					FT FT
FT					NON-TER 105 105
FT					NON-TER 105 AA; 11882 MW; 6ECH6C02CD30EFA2 CRC64;
SQ					SEQUENCE 105 AA; 105
Query Match	24.9%; Score 445; DB 4; Length 105;				Query Match 24.9%; Score 445; DB 4; Length 105;
Best Local Similarity	72.5%; Pred. No. 4.7e-32;				Best Local Similarity 72.5%; Pred. No. 4.7e-32;
Matches	12; Mismatches 16; Indels 0; Gaps 0;				Matches 74; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
QY	112 PTEQTPVYRQCYHGNGQSYRGTGSTTVTGRTCQSWSSMTPHRHORTPNDGLTNYC 171				QY 112 PTEQTPVYRQCYHGNGQSYRGTGSTTVTGRTCQSWSSMTPHRHORTPNDGLTNYC 171
Db	1 PTEQSPGVQDCYHGDSQRSGTSFSTVYAPPTV 213				Db 1 PTEQSPGVQDCYHGDSQRSGTSFSTVYAPPTV 213
QY	172 RNPDAEGRGPFETDPSIRWECLNLRCSDEGYVVAPEPTV 213				QY 172 RNPDAEGRGPFETDPSIRWECLNLRCSDEGYVVAPEPTV 213
Db	61 RNPDAEISPWNCYTDPNVREWCNLICQCPVTESSYLAISTAV 102				Db 61 RNPDAEISPWNCYTDPNVREWCNLICQCPVTESSYLAISTAV 102
SEQUENCE	285 AA;				RESULT 12
SQ	285 AA;				Q9N1B8 PRELIMINARY; PRT; 109 AA.
Query Match	26.1%; Score 466; DB 4; Length 285;				ID Q9N1B8 ID Q9N1B8
Best Local Similarity	43.1%; Pred. No. 2.1e-33;				AC Q9N1B8
Matches	85; Conservative 21; Mismatches 51; Indels 40; Gaps 4;				DT 01-OCT-2000 (TRIMBUREL 15, Created)
QY	5 VQDCYHGDGRAYRGISSTTVGRTCQSWSSMIPMHQRTPEVNPGNLTNYCRNPDSGK 64				DT 01-OCT-2000 (TRIMBUREL 15, Last sequence update)
Db	125 IRNCLICKGRAYKGKVLSITKSGIKCQEWSSMIPHEH----SYRGKDQENYCNP-RGE 178				DT 01-MAR-2003 (TRIMBUREL 23, Last annotation update)
Qy	65 Q--PWCVTTDPCVRAEYCNLTQCSSETESGVLETPIVVPVPSMAHSAAPIEQPVVRQC 122				DE Hepatocyte growth factor (Fragment).
Db	179 EGGEFWCEISNFEEVYEVCDIPOQSEVE-----C 206				DN GNF
Qy	123 YHGNGQSYRGTGSTTVTGRTCQSWSSMTPHRHORTPNDGLTNYCNPDAATGFWC 182				OS Ovis aries (Sheep).
Db	207 MTENGESTRGLMDHESGKTCQRWDQTHPRHKPFPERYPDGFDDNYCRNPDQSPFWC 266				OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Caprine; Ovis. NCBI_TAXID=940;
QY	183 FTTDPSTIRWEWCNLTRC 199				RN [1]
Db	267 YTLDPHTPWECAIRTC 283				SEQUENCE FROM N.A.
RP					RC TISSUE=Endometrium;
RC					MEDLINE:2029/031; PubMed=10819791;
RX					RA Chen C., Spencer T.E., Bazer F.W.; "Expression of hepatocyte growth factor and its receptor c-met in the ovine uterus." Biol. Reprod. 62:1844-1850(2000).
RL					-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

DR	01-JUN-2001	(TRIMBrel_17, Last sequence update)
DT	01-MAR-2003	(TRIMBrel_23, Last annotation update)
DE	Hepatocyte growth factor (Fragment).	
GN	HGF.	
PRAM	Homo sapiens (Human).	
PSR	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TAXID	9606;	
[1]		
SEQUENCE FROM N.A.		
RX	Medline=9136928; PubMed=1832556;	
RA	Niyazawa K., Kitamura A., Kitamura N.:	
RT	"Structural organization and the transcription initiation site of the human hepatocyte growth factor gene."	
RL	Biochemistry 30:9170-9176(1991).	
CC	-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.	
DR	EMBL: M75367; AAG53459.1; JOINED.	
DR	EMBL: M75366; AAG53459.1; JOINED.	
DR	EMBL: M75368; AAG53459.1; JOINED.	
DR	EMBL: M75369; AAG53459.1; JOINED.	
HSSP	PL4210; IBHT.	
DR	InterPro; IPR000001; Kringle.	
DR	InterPro; IPR003014; PAN.	
DR	InterPro; IPR003609; Pan_APP.	
PRAM	IPR003966; Prothrombin.	
PRAM	Pf00024; PAN_1.	
PRINTS	PRO00018; KRINGLE.	
PRINTS	PRO1505; PROTHROMBIN.	
PRODOM	PD000335; Kringle_1.	
SMART	SM00130; KR_1.	
SMART	SM00473; PAN_AP_1.	
PROSITE	PS00021; KRINGLE_1;	
PROSITE	PS50070; KRINGLE_2;	
KW	Glycoprotein; Kringle.	
FT	NON_TER 208 AA; 23931 MW;	
SQ	AEGC50DE3A6B37P CRC64;	
Query Match 14.6%; Score 261.5%; DB 6; Length 109;		
Best Local Similarity 39.0%; Pred. No. 9.1e-16;		
Matches 48; Conservative 15; Mismatches 37; Indels 23; Gaps 2;		
QY 114 BOPPVYRQCHNGQSYINGFSTVIGRTQCSWSMTHQRTPENYPNDGLTANYCRN 173		
Db 9 ENKDLRNCLIGKGSYKGTVSTKSIGKCPWNNSMIPHEHSLFLPSYRGKDQENYCRN 68		
QY 174 PDAAT-GPWCETTDPLTNTROSDFEGTVAAPTVIVPSLGPSEQDCMFNGNCK 232		
Db 69 PRGEEGGPWCETSNPEVRYEVCDIPQCSEVE-----CMTCNGE 106		
QY 233 GYR 235		
Db 107 SYR 109		
RESULT 13		
Q8BS17	PRELIMINARY;	
ID Q8BS17,	PRT;	
AC Q8BS17,	209 AA.	
DT 01-MAR-2003 (TRIMBrel_23, Created)		
DT 01-MAR-2003 (TRIMBrel_23, Last sequence update)		
DT 01-MAR-2003 (TRIMBrel_23, Last annotation update)		
DE Plasmidgen.		
OS Mus musculus (Mouse).		
Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.		
NCBI_TAXID=10090;		
RX	SEQUENCE FROM N.A.	
STRAIN=5757B/60; TISSUE=Aorta and vein;		
MEDLINE=22334683; PubMed=12466851;		
RA	The RANTOM Consortium,	
RA	"Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs."	
RT	Nature 420:563-573 (2002).	
DR	AK040840; BAC3711.1; -.	
SQ	SEQUENCE 209 AA; 23192 MW; FA5880C13A7FABE7 CRC64;	
Query Match 14.5%; Score 260; DB 11; Length 209;		
Best Local Similarity 44.3%; Pred. No. 2.6e-15;		
Matches 47; Conservative 15; Mismatches 42; Indels 2; Gaps 2;		
QY 114 EQTPVVYRQCHNGQSYRHFSTVIGRTQCSWSMTHQRTPENYPNDGLTANYCRN 173		
Db 95 EKRYVLECKKGIGGNGYRGTMSRTKSGYACQWQGATPHPNVSPSPHNEGLGENYCRN 154		
QY 174 PDAD-TGPWCETTDPLTNTROSDFEGTVAAPTVIVPSL 218		
Db 155 PDNDEQFWCTTDPKRYCN1PECEGRGGs-RKPPSTCLSPGI 199		
RESULT 14		
Q9BYM0	PRELIMINARY;	
ID Q9BYM0	PRT;	
AC Q9BYM0;	208 AA.	
DT 01-JUN-2001 (TRIMBrel_17, Created)		
DB	SEQUENCE FROM N.A.	
RX	Medline=96278713; PubMed=8652798;	
RA	Cioce V., Csaky K.G., Chan A.M.L., Bottaro D.P., Taylor W.G.,	
RA	Jensen R., Aaronson S.A., Rubin J.S.;	
RT	"Hepatocyte growth factor (HGF)/NK1 is a naturally occurring	
RT	HGF/scatter factor variant with partial agonist/antagonist activity."	
RL	J. Biol. Chem. 271:13110-13115 (1996).	
CC	-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.	
RESULT 15		
Q13494	PRELIMINARY;	
TD 0113494	PRT;	
AC	210 AA.	
DT 01-NOV-1996 (TRIMBrel_01, Created)		
DT 01-NOV-1996 (TRIMBrel_01, Last sequence update)		
DT 01-MAR-2003 (TRIMBrel_23, Last annotation update)		
DE	HGF agonist/antagonist.	
OS Homo sapiens (Human).		
RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TAXID=9606;		
[1]		
RN	SEQUENCE FROM N.A.	
RX	Medline=96278713; PubMed=8652798;	
RA	Cioce V., Csaky K.G., Chan A.M.L., Bottaro D.P., Taylor W.G.,	
RA	Jensen R., Aaronson S.A., Rubin J.S.;	
RT	"Hepatocyte growth factor (HGF)/NK1 is a naturally occurring	
RT	HGF/scatter factor variant with partial agonist/antagonist activity."	
RL	J. Biol. Chem. 271:13110-13115 (1996).	
CC	-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.	

	DR	EMBL; U46010; AAC50539.1;	-
DR	HSSP; PI4210; IBHT.		
DR	InterPro; IPR000001; Kringle.		
DR	InterPro; IPR003014; PAN.		
DR	InterPro; IPR03609; Pan_app.		
DR	Pfam; PF00051; kringle_1.		
DR	Pfam; PF0024; PAN_1.		
DR	ProDom; PD000395; Kringle_1.		
DR	SMART; SM00130; KR_1.		
DR	SMART; SM00473; PAN_AP_1.		
DR	PROSITE; PS00021; KRINGLE_1.		
DR	PROSITE; PS00070; KRINGLE_2_1.		
KW	Glycoprotein; Kringle; 1.		
SEQUENCE	210 AA;	24116 MN;	94A6EE9C50DE5A86 CRC64;
Query Match	14.0%	Score 249.5;	DB 4;
Best Local Similarity	47.2%	Length 210;	
Matches	42;	Pred. No. 2.3e-14;	
	Conservative	Mismatches 32;	Indels 1;
		Gap 1;	
QY	114 EQFPVVROCYHNGQSYRGTFSTVGTICQWSWMMTPHRQRPFENPNPDGLTMNYCRN 173		
Db	120 ENDYIRNCITGKGRYKGTVSKGKCPWSSMTPHEHSFFPSSYRKDQLQENCRN 179		
QY	174 PADD-GPWCFSTDPSIRKTYCNLTRCD 201		
Db	180 PRGEEGFWCFTSNPVRYEVCDIFQCSE 208		

Result No.	Score	Query Match Length DB ID	Description
1	539	100.0 91 22 PAF72945	Human apolipoprotein(a) kringle domain IV36, LK6 protein.
2	405	77.0 90 21 AAB01909	Human apolipoprotein(a) kringle domain IV36, LK6 protein.
3	405	75.1 84 21 AAY77220	Human apolipoprotein(a) kringle domain IV36, LK6 protein.
4	402	74.6 89 22 PAF72946	Human apolipoprotein(a) kringle domain IV36, LK6 protein.
5	397	73.7 82 10 AAF92231	Plasminogen Kringle 1
6	383	71.1 78 17 AAW07560	Human Kringle 4.
7	377	69.9 83 21 AAB02414	Amino acid sequence of Human ORFX protein.
8	350	64.9 78 17 AAW07559	Murine Kringle 4.
9	339	63.0 86 23 ABP02801	Human ORFX protein.

XX Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis; has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -
XX Claim 1; Page 44-45; 50pp; English.
XX The present sequence is human LK6 protein which contains the amino
CC acid sequence of human apolipoprotein(a) kringle domain IV36
CC (KITV36). The human apolipoprotein(a) kringle domains IV36 (LK6
CC protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
CC angiogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are
CC inhibitors are of endothelial cell proliferation, cell migration and
CC normal development of capillaries in the chick embryo chorionallantoic
CC membrane (CAM). LK68 protein, its single kringles or their functional
CC equivalents, are useful for treating angiogenesis-mediated diseases,
CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC disease in animals or humans. LK68 is useful as an anticancer agent and
CC also for inhibiting primary tumour growth.

XX Sequence 91 AA;
Query Match 100.0%; Score 539; DB 22; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.5e-42; Indels 0; Gaps 0;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ Sequence 90 AA;

```

Qy 1 KSPVYQDCYHGDGRSYRGISSTIVGTCQSMSSMIPWHQRPENPNAGLTENYCNP 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 KSPVYQDCYHGDGRSYRGISSTIVGTCQSMSSMIPWHQRPENPNAGLTENYCNP 60

```

```

Qy 61 DSGKQFQCYTIDPCYRWECLNLTQCSSETESG 91
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 DSGKQFQCYTIDPCYRWECLNLTQCSSETESG 91

```

RESULT 2
ID AAB01909 standard; protein; 90 AA.

XX AAB01909;

XX DT 18-SEP-2000 (first entry)

DB Human plasminogen kringle 4 (Val354-Val443).

XX Plasminogen; human; kringle domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antipsoriatic; antiinflammatory; antiluler; antirheumatic; antiarthritic;
KW antiangiogenic; cancer; tumour; autoimmune disease.
XX Homo sapiens.

XX US6057122-A.

XX PD 02-MAY-2000.

XX PF 05-MAY-1997; 97US-0851350.

XX PR 03-MAY-1996; 96US-0643319.

XX PR 03-APR-1997; 97US-0832087.

XX PA (ABBO) ABBOTT LAB.

XX PI Davidson DJ;

XX DR WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer,
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation -
XX

PS Example 17; Page -; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
CC peptide fragments. The method comprises mixing mammalian plasminogen and
CC elastase in the ratio 1:10-1:300, followed by incubating and isolating
CC the fragment. The Kringle 5 peptides are inhibitors of angiogenesis and
CC endothelial cell proliferation and migration. The peptides are useful
CC for treating angiogenic diseases, primary and metastatic solid tumours
CC and carcinomas of various organs such as breast, genital tract,
CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
CC arising from haemopoietic malignancies such as leukaemias and
CC lymphomas. They are also used for the prophylaxis of various autoimmune
CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Weber-
CC Syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
CC in an exemplification of the invention.

CC Note: This sequence is not shown in the specification, but is derived
CC from the full length human plasminogen sequence (AAB01887) shown in
CC figure 1.

XX Sequence 90 AA;

```

Query Match 3 77.0%; Score 415; DB 21; Length 90;
Best Local Similarity 79.3%; Pred. No. 4.1e-31.
Matches 69; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
SQ Sequence 90 AA;
```

```

Qy 4 VVQDCYHGDGRSYRGISSTIVGTCQSMSSMIPWHQRPENPNAGLTENYCRNPDSG 63
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 VVQDCYHGDGRSYRGISSTIVGTCQSMSSMIPWHQRPENPNAGLTENYCRNPDSG 60

```

```

Qy 64 KQPWCYTIDPCYRWECLNLTQCSSETESG 90
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 KGPNCFTIDPSYRWECLNKKCSSTEA 87

```

RESULT 3

AAY77720

XX standard; protein; 84 AA.

XX ID AAY77720

XX AC AAY77720

XX DT 12-MAY-2000 (first entry)

XX DE Human plasminogen kringle 4 sequence.

XX Kringle 4: plasminogen; anti-angiogenic; angiogenesis; angiotatin;
KW cytosatic; antiatherosclerotic; antidiabetic; antihypertensive;
KW immunosuppressant; vasoactive; vunlear; dermatological; human;
KW dermatological; cancer; tumour; birth control; vascularization.

XX OS Homo sapiens.

XX PN WO200003726-A1.

XX PD 27-JUN-2000.

XX Key

XX Region 59..75

XX FT /note= "specifically claimed fragment (AAY77723)"

XX PR 14-JUL-1998;

XX PN 96US-0092831.

XX (BRII) BRISTOL-MYERS SQUIBB CO.

XX PI JI R, Trail PA;

DR WPI; 2000-171200/15.
 XX DR WPI; 2001-244787/25.
 PT DR N-PSDB; AAD03757.
 PT Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
 PT diseases, e.g. cancer and rheumatoid arthritis, has human
 PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
 PT sequence -
 XX Disclosure; Fig 3; 30pp; English.
 XX
 CC The invention provides fragments of kringle 1, 2 or 4 of human
 CC plasminogen that contain a lysine binding site and have anti-angiogenic
 CC activity. The peptides of the invention function as antiangiogenic
 CC agents, for the treatment process and diseases involving angiogenesis.
 CC such diseases include cancers such as solid tumours, blood born tumours
 CC such as leukemias, tumours metastasis, benign tumours such as
 CC hemangiomas, acoustic acuromas, neurofibromas, trachomas and pyogenic
 CC granulomas, rheumatoid arthritis, ocular angiogenic diseases such as
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubella, Osler-Webber syndrome, myocardial angiogenesis, plaque
 CC neovascularization, telangiectasia, hemophilic joints, angiofibroma,
 CC and wound granulation. The fragments are also useful in treatment of
 CC disease of excessive or abnormal stimulation of endothelial cells. These
 CC diseases include intestinal adhesions, atherosclerosis, scleroderma, and
 CC hypertrophic scars. The fragments can be used as birth control agents by
 CC preventing vascularization required for embryo transplantation. The
 CC present sequence represents the kringle 4 sequence of human plasminogen
 CC (angiostatin).
 XX Sequence 84 AA;
 Query Match 75.1%; Score 405; DB 21; Length 84;
 Best Local Similarity 79.3%; Pred. No. 3.2e-10;
 Matches 67; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 QY 5 VQDCYHGDDGSRGTSSTVGRFCQSWSMIPHWHORTPENYCRNPDSGK 64
 DB 1 VQDCYHGDDGQSRGTSSTVGRFCQSWSMIPHWHORTPENYCRNPDADK 60
 QY 65 QPWYTTTPCVCWYENLNLTQSET 88
 DB 61 GPWCETTDSEVWYCNLKKSGT 84
 RESULT 4
 AAY72946 ID AAY72946 standard; Protein; 89 AA.
 XX AC AAY72946;
 XX DT 13-JUN-2001 (first entry)
 DE Human apolipoprotein(a) kringle domain IV37, LK7 protein.
 KW Human; angiogenesis inhibitor; LK7; apolipoprotein(a) kringle domain;
 KW angiogenesis mediated disease; cancer; rheumatoid arthritis; therapy;
 KW cytostatic; antiinflammatory; antiarthritic; antipsoriatic; psoriasis;
 KW ocular angiogenic disease; endothelial cell proliferation; tumour;
 KW cell migration.
 OS Homo sapiens.
 PN WO200119858-A1.
 XX PD 22-MAR-2001.
 XX PF 15-SEP-1999; 99WO-KR00554.
 XX PR 15-SEP-1999; 99WO-KR00554.
 XX PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
 XX PI Chang J, Kim JS, Park EI, Yum J, Chung S;

XX DR WPI; 2001-244787/25.
 XX DR N-PSDB; AAD03757.
 PT Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
 PT diseases, e.g. cancer and rheumatoid arthritis, has human
 PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
 PT sequence -
 XX
 PS Claim 2; Page 45-46; 50pp; English.
 XX
 CC The present sequence is human LK7 protein which contains the amino
 CC acid sequence of human apolipoprotein(a) kringle domain IV37
 CC (LK7). The human apolipoprotein(a) kringle domains IV36 (LK6
 CC protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
 CC angiogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are
 CC inhibitors are of endothelial cell proliferation, cell migration and
 CC normal development of capillaries in the chick embryo chorioallantoic
 CC membrane (CAM). LK68 protein, its single kringles or their functional
 CC equivalents, are useful for treating angiogenesis mediated diseases,
 CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
 CC disease in animals or humans. LK68 is useful as an anticancer agent and
 CC also for inhibiting primary tumour growth.
 XX Sequence 89 AA;
 Query Match 74.6%; Score 402; DB 22; Length 89;
 Best Local Similarity 77.6%; Pred. No. 6.5e-30;
 Matches 66; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 5 VQDCYHGDDGSRGTSSTVGRFCQSWSMIPHWHORTPENYCRNPDGSK 64
 DB 1 VQDCYHGDDGSRGTSSTVGRFCQSWSMIPHWHORTPENYCRNPDADK 60
 QY 65 QPWYTTTPCVCWYENLNLTQSET 89
 DB 61 GPWCETTDSEVWYCNLKKSGT 85
 RESULT 5
 AAP93231 ID AAP93231 standard; peptide; 82 AA.
 XX AC AAP93231;
 XX DT 25-MAR-2003 (updated)
 DT 03-APR-1990 (first entry)
 XX Plasminogen kringle 4 domain (residues 354-435).
 DE XX
 KW XX Plasminogen; activator; t-Pa; fibrin; kringle domain;
 KW scu PA;
 KW XX
 OS XX Homo sapiens.
 PN WO8910401-A.
 XX PD 02-NOV-1989.
 XX PR 23-MAR-1989; 89WO-US01255.
 XX PR 22-APR-1988; 88US-0184823.
 XX PA (COLIB) COLLABORATIVE RES INC.
 XX PI Mao JI, Abercrombie DM;
 XX DR WPI; 1989-339955/46.
 DR N-PSDB; AAN2238.
 XX PT Modified plasminogen activator - having greater fibrin
 PT selectivity and circulating halflife.
 XX

PS Disclosure; fig 3b; 80pp; English.
 XX The sequence is encoded by a synthetic oligonucleotide and is the kringle
 CC 4 domain of plasminogen. It is used to construct a modified plasminogen
 CC activator (mPA) of greater fibrin selectivity than normal PA. The mPA is
 CC used in the treatment of pulmonary embolism, thrombosis, myocardial
 CC infarct and strokes.
 CC (updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 82 AA;
 SQ Query Match 73.7%; Score 397; DB 10; Length 82;
 Best Local Similarity 79.3%; Pred. No. 1.7e-29;
 Matches 65; Conservative 7; Gaps 0;
 Indels 0;
 QY 4 VYQDCYFGDGRSYNGISSLTTVGRTOQSWSMTHQRTPEVNPAIGLTDENYCRNPDSG 63
 Db 1 VYQDCYHGNGSYRTTSSITTGKKCQSWSSMTPHRHQKTPENPVNAGLMNYCRNPAD 60
 QY 64 KQFWCYTIDPQVRYCNITQC 85
 Db 61 KGFWCFTIDPSVRYCNITKC 82

RESULT 6
 AAW07560
 ID AAW07560 standard; protein; 78 AA.
 AC AAW07560;
 XX DT 22-JUN-1997 (first entry)
 XX DB Human kringle 4.
 XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 KW macular degeneration; diabetic retinopathy.
 XX Homo sapiens.
 OS PN WO9635774-A2.
 XX PD 14-NOV-1996.
 XX PF 26-APR-1996;
 XX 96WO-US05856.
 PR 08-MAR-1996;
 PR 96US-0612788.
 PR 26-APR-1995;
 PR 95US-0429743.
 PR 22-FEB-1996;
 PR 96US-0605598.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;
 XX DR WPI; 1996-518662/51.
 XX PT Use of angiostatin fragments or aggregates - for inhibiting
 PT endothelial cell proliferation and treating angiogenesis-mediated
 PT diseases, e.g. cancer, arthritis or diabetic retinopathy
 XX PS Claim 4; Page 116; 203pp; English.
 XX The invention relates to new methods and compositions for
 CC inhibiting endothelial cell proliferation, using as active component
 CC an angiostatin fragment, a combination of angiostatin fragments, or
 CC aggregate angiostatin. The fragment is preferably derived from murine,
 CC human, Rhesus, Porcine or bovine Plasminogen and is a kringle 1,
 CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
 CC 1-4 or kringle 1-4BULS protein. The aggregate angiostatin has a Mol. wt.
 CC of 45-65 kD and is derived from a plasminogen fragment beginning at
 CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
 CC bovine plasminogen. The active component can be used for treating
 CC angiogenesis-mediated diseases such as cancer, arthritis, macular
 CC degeneration and diabetic retinopathy. It can also be used to develop

CC antibodies for use in diagnosis, detection and therapy.
 CC The present sequence, human kringle 4, is a specific angiostatin
 CC fragment which can be used in the invention.
 XX SQ Sequence 78 AA;
 Query Match 71.1%; Score 303; DB 17; Length 78;
 Best Local Similarity 79.3%; Pred. No. 3.2e-28;
 Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 QY 8 CYHGDGRSYRGLISSTVTGRTQCSWSSMIPWHQRTPEVNPAIGLTDENYCRNPDSGKPW 67
 Db 1 CYHGDGSQSTGTSSTTGKKCQSWSSMTPHRHQKTPENPVNAGLMNYCRNPADKGWP 60
 QY 68 CYTDPYCVRWEYCNITQC 85
 Db 61 CFTDPSVRYCNITKC 78
 RESULT 7
 AAB08414
 ID AAB08414 standard; protein; 83 AA.
 XX AAB08414;
 AC AAB08414;
 XX DT 20-DEC-2000 (first entry)
 XX DE Amino acid sequence of kringle 4 of human plasminogen.
 XX KW Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA;
 KW tissue plasminogen activator; tumour; atherosclerosis; arthritis;
 KW retinopathy; bronchial vascular congestion; inflammatory bowel disease;
 KW adult respiratory distress syndrome; Castleman's disease; psoriasis;
 KW hepatitis; aneurysm; renal disease; haemangioma.
 XX Homo sapiens.
 OS PN WO200049871-A1.
 XX PD 31-AUG-2000.
 XX PF 24-FEB-2000; 2000WO-US04798.
 XX PR 24-FEB-1999; 99US-0121341.
 PR 25-FEB-1999; 99US-0121633.
 PR 18-NOV-1999; 99US-0166176.
 XX PA (FORD-) FORD HEALTH SYSTEM HENRY.
 XX PI Dou D, Chopp M, Wang L, Mikkelsen T;
 XX DR WPI; 2000-572016/53.
 XX PT Use of kringle protein and kringle proteins derived from plasminogen and
 PT composition comprising kringle proteins for treating tumor and
 PT atherosclerosis, arthritis and retinopathy -
 XX PS Disclosure; Fig 6; 16pp; English.
 CC The specification describes a human polypeptide which is a potent
 CC angiogenesis inhibitor, and is designated KED. KED polypeptide, kringle
 CC proteins, or a kringle derived from human tissue plasminogen activator
 CC (tPA) protein are used to inhibit angiogenesis; Kringle protein, KED
 CC arthritis, retinopathy and other similar diseases. KED is also useful
 CC for the treatment of diseases such as bronchial vascular congestion,
 CC inflammatory bowel disease, adult respiratory distress syndrome,
 CC Castleman's disease, psoriasis, hepatitis, aneurysm, renal disease,
 CC and haemangioma. The present sequence represents kringle 4 of human
 CC plasminogen, which is used in the course of the invention.
 XX SQ Sequence 83 AA;

QY	8	CYHGDGSTRG IISSTIVTGRPCQSNSMTPHHWORTPNYPAGLITENYCRNPSPGKWP	67
Db	1	CYQSGDQSTRGTTSTTGKRCQSWAAMPFRHSKTPENPDAGLEMMNYCRNPQGDCKPW	60
QY	68	CYTIDDCVKEYCNLTCQ	85
Db	61	CYTIDDSVRYCNLKC	78
RESULT	9		
	ABP02801	standard; Protein: 86 AA.	
	XX		
	AC	ABP02801;	
	XX		
	DT	24-JUN-2002 (first entry)	
	XX		
DE	Human ORFX protein sequence SEQ ID NO:5584.		
XX			
KW	Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200192523-A2.		
XX			
PD	06-DEC-2001.		
XX			
PF	29-MAY-2001; 2001WO-US10836.		
XX			
PR	30-MAY-2000; 2000US-206132P.		
PR	29-AUG-2000; 2000US-228716P.		
XX			
PA	(CURA-) COURAGE CORP.		
XX			
PI	Shimkets RA, Leach MD;		
XX			
DR	WPI: 2002-106308/14.		
DR	N-PSDB; ABN18553.		
XX			
PT	Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.		
PT			
XX			
PS	Disclosure; SEQ ID 5584; 1037pp; English.		
XX			
CC	The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN2752 encode the human ORFX proteins given in ABP0010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis, of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX Proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis.		
CC	Conformational variants, splicing variants, fusion and conditions resulting from		

CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://ftplib.wipo.int/pub/published_pct_sequences](http://ftplib.wipo.int/pub/published_pct_sequences).

SQ Sequence 86 AA;

RESULT 10

AAW07554 ID AAW07554 standard; protein; 78 AA.

XX AC AAW07554;

XX DT 21-JUN-1997 (first entry)

DE Murine kringle 3.

XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 macular degeneration; diabetic retinopathy.

XX OS Mus musculus.

XX PN WO9635774-A2.

XX PD 14-NOV-1996.

XX PF 26-APR-1996; 96WO-US03856.

XX PR 08-MAR-1996; 96US-0612788.

XX PR 26-APR-1995; 95US-0429743.

XX PR 22-FEB-1996; 96US-0605598.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;

XX DR WPI; 1996-518662/51.

XX PS Use of angiostatin fragments or aggregates - for inhibiting
 endothelial cell proliferation and treating angiogenesis-mediated
 diseases, e.g. cancer, arthritis or diabetic retinopathy

PT PS Claim 4; Page 111; 203pp; English.

XX The invention relates to new methods and compositions for
 inhibiting endothelial cell proliferation, using as active component,
 an angiostatin fragment, combination of angiostatin fragments, or
 aggregate angiostatin. The fragment is preferably derived from murine,
 human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
 kringle 2, kringle 3, kringle 2-3, kringle 1-2, kringle
 1-4 or kringle 1-4BKLS protein. The aggregate angiostatin has a Mol. Wt.
 of 45-65 kD and is derived from a plasminogen fragment beginning at
 approximately amino acid number 98 of murine, human, Rhesus, porcine or
 bovine plasminogen. The active component can be used for treating
 angiogenesis-mediated diseases such as cancer, arthritis, macular
 degeneration and diabetic retinopathy. It can also be used to develop
 antibodies for use in diagnosis, detection and therapy.

CC The present sequence, murine kringle 3, is a specific angiostatin
 fragment which can be used in the invention, and represents amino
 acids 275-352 of murine plasminogen or amino acids 178-255 of murine

CC fragment which can be used in the invention, and represents amino
 acids 178-255 of human angiostatin.

CC Sequence 78 AA;

RESULT 11

AAW07555 ID AAW07555 standard; protein; 78 AA.

XX AC AAW07555;

XX DT 21-JUN-1997 (first entry)

DE Human kringle 3.

XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 macular degeneration; diabetic retinopathy.

XX OS Homo sapiens.

PN WO9635774-A2.

XX PD 14-NOV-1996.

XX PF 26-APR-1996; 96WO-US03856.

XX PR 08-MAR-1996; 96US-0612788.

XX PR 26-APR-1995; 95US-0429743.

XX PR 22-FEB-1995; 96US-0605598.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;

XX DR WPI; 1996-518662/51.

XX PS Use of angiostatin fragments or aggregates - for inhibiting
 endothelial cell proliferation and treating angiogenesis-mediated
 diseases, e.g. cancer, arthritis or diabetic retinopathy

PT PT PS Claim 4; Page 112; 203pp; English.

XX The invention relates to new methods and compositions for
 inhibiting endothelial cell proliferation, using as active component,
 an angiostatin fragment, a combination of angiostatin fragments, or
 aggregate angiostatin. The fragment is preferably derived from murine,
 human, Rhesus, Porcine or bovine Plasminogen and is a kringle 1,
 kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
 1-4 or kringle 1-4BKLS protein. The aggregate angiostatin has a Mol. Wt.
 of 45-65 kD and is derived from a plasminogen fragment beginning at
 approximately amino acid number 98 of murine, human, Rhesus, porcine or
 bovine Plasminogen. The active component can be used for treating
 angiogenesis-mediated diseases such as cancer, arthritis, macular
 degeneration and diabetic retinopathy. It can also be used to develop
 antibodies for use in diagnosis, detection and therapy.

CC The present sequence, human kringle 3, is a specific angiostatin
 fragment which can be used in the invention, and represents amino
 acids 178-255 of human angiostatin.

CC Sequence 78 AA;

Query Match	52.18;	Score 281;	DB 17;	Length 78;	QY	8 CYHGDRGSYRGISSTTVGRTTCOSWSSMIPHWHQRTPENYPNAGLITENYCRNPDSKGKQFW 67
Best Local Similarity	56.4%;	Pred. No.	8.6e-19;		Db	1 CLKTGIGNYRQDVATVTSWHTCHGWSAQTPATHNKTTPENPKRNLDENYCRNPDSGEKAW 60
Matches	44;	Conservative	10;	Mismatches 24;	Indels 0;	Gaps 0;
QY	8 CYHGDRGSYRGISSTTVGRTTCOSWSSMIPHWHQRTPENYPNAGLITENYCRNPDSKGKQFW 67				QY	68 CYTDDPCYRVEYNLCNLTQC 85
Db	1 CLKTGIGNYRQDVATVTSWHTCHGWSAQTPATHNKTTPENPKRNLDENYCRNPDSGEKAW 60				Db	61 CTTTNSQYRWEYCKIPSC 78
QY	68 CYTDDPCYRVEYNLCNLTQC 85				RESULT 13	
Db	61 CTTTNSQYRWEYCKIPSC 78				ID AAW07557	AAW07557 standard; protein; 78 AA.
RESULT 12					XX	
AAW07556					AC AAW07557;	AC
ID AAW07556 standard; protein; 78 AA.					XX	XX
XX					DT 21-JUN-1997	(first entry)
AC					XX	
AAW07556;					DE Porcine Kringle 3.	
XX					XX	
DT 21-JUN-1997	(first entry)				DE	
XX					XX	
DE Rhesus kringle 3.					DE	
XX					XX	
KW angiostatin; Plasminogen; kringle; angiogenesis; cancer; arthritis;					XX	
XX macular degeneration; diabetic retinopathy.					OS Sus scrofa.	
XX Rhesus.					XX	
OS					PN WO935774-A2.	
XX					XX	
PN WO935774-A2.					PD 14-NOV-1996.	
XX					XX	
14-NOV-1996.					PP 26-APR-1996;	96WO-US05856.
PD					XX	
XX 14-NOV-1997	(first entry)				PR 08-MAR-1996;	96US-0612788.
DE					PR 26-APR-1995;	95US-0423743.
XX Rhesus kringle 3.					PR 22-FEB-1995;	96US-060598.
KW					XX (CHIL-) CHILDRENS MEDICAL CENT.	
XX angiostatin; Plasminogen; kringle; angiogenesis; cancer; arthritis;					XX PA Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;	
XX macular degeneration; diabetic retinopathy.					XX PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;	
XX OS					XX XX WPI: 1996-518662/51.	
XX Rhesus.					XX XX Use of angiostatin fragments or aggregates - for inhibiting	
XX					PT endothelial cell proliferation and treating angiogenesis-mediated	
XX					PT diseases, e.g. cancer, arthritis or diabetic retinopathy	
14-NOV-1996.					XX XX Claim 4: Page 113-114; 203pp; English.	
PD					XX XX The invention relates to new methods and compositions for	
XX 26-APR-1995;					CC inhibiting endothelial cell proliferation, using as active component	
PR					CC an angiostatin fragment, a combination of angiostatin fragments, or	
XX 26-APR-1995;					CC aggregate angiostatin. The fragment is preferably derived from murine,	
PR					CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,	
XX 22-FEB-1995;					CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle	
PR					CC 1-4 or kringle 1-4-BKLs protein. The aggregate angiostatin has a Mol. Wt.	
XX 22-FEB-1995;					CC of 45-65 kD and is derived from a plasminogen fragment beginning at	
PR					CC approximately amino acid number 98 of murine, human, Rhesus, porcine or	
XX 96US-060598.					CC bovine plasminogen. The active component can be used for treating	
PA (CHIL-) CHILDRENS MEDICAL CENT.					CC angiogenesis-mediated diseases such as cancer, arthritis, macular	
XX					CC degeneration and diabetic retinopathy. It can also be used to develop	
PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;					CC antibodies for use in diagnosis, detection and therapy.	
XX					CC The present sequence, porcine kringle 3, is a specific angiostatin	
DR WPI: 1996-518662/51.					CC fragment which can be used in the invention, and represents amino	
XX					CC acids 178-255 of porcine angiostatin.	
PT use of angiostatin fragments or aggregates - for inhibiting					XX SQ Sequence 78 AA;	
PT endothelial cell proliferation and treating angiogenesis-mediated					Query Match Score 278; DB 17; Length 78;	
PT diseases, e.g. cancer, arthritis or diabetic retinopathy					Best Local Similarity 57.7%; Pred. No. 1.6e-18;	
XX					Mismatches 6; Indels 27;	
XX 112-113; 203pp; English.					Db 0; Gaps 0;	
PS						
XX The invention relates to new methods and compositions for						
XX inhibiting endothelial cell proliferation, using as active component						
CC an angiostatin fragment. The fragment is preferably derived from murine,						
CC aggregate angiostatin. The fragment is preferably derived from murine,						
CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,						
CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle						
CC 1-4 or kringle 1-4-BKLs protein. The aggregate angiostatin has a Mol. Wt.						
CC of 45-65 kD and is derived from a plasminogen fragment beginning at						
CC approximately amino acid number 98 of murine, human, Rhesus, porcine or						
CC bovine plasminogen. The active component can be used for treating						
CC angiogenesis-mediated diseases such as cancer, arthritis, macular						
CC degeneration and diabetic retinopathy. It can also be used to develop						
CC antibodies for use in diagnosis, detection and therapy.						
CC The present sequence, porcine kringle 3, is a specific angiostatin						
CC fragment which can be used in the invention, and represents amino						
CC acids 178-255 of porcine angiostatin.						
XX SQ Sequence 78 AA;						
Query Match Score 281; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 8.6e-19;						
Matches 45; Conservative 7; Mismatches 26; Indels 0;						
SQ Sequence 78 AA;						
Query Match Score 281; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 8.6e-18;						
Matches 45; Conservative 7; Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 0; Gaps 0;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 0; Gaps 0;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;						
SQ Sequence 78 AA;						
Query Match Score 278; DB 17; Length 78;						
Best Local Similarity 57.7%; Pred. No. 1.6e-18;						
Mismatches 6; Indels 27;				</td		

GenCore version 5.1.6
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:18:25 ; search time 29 Seconds
(without alignment times)
132.769 Million cell updates/sec

Title: US-10-088-548-4

Perfect score: 539

Sequence: 1 RSPVYODCYHGDGRSYRIS.....DPCVRWEYCNLQCSETESG 91.

Scoring table: BL05UM62

Gapext 0.5

Searched: 32817 seqs 42310858 residues

Total number of hits satisfying chosen parameters:

224404

Minimum DB seq length: 0
Maximum DB seq length: 91

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/1/aa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/1/aa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/1/aa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/1/aa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/1/aa/PCUTUS_COMB.pep:
6: /cgn2_6/ptodata/1/1/aa/backfile1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	405	75.1	84	4	US-09-348-953-2	Sequence 2, Appli
2	383	71.1	78	2	US-08-612-788-23	Sequence 23, Appli
3	383	71.1	78	2	US-08-763-528A-5	Sequence 5, Appli
4	383	71.1	78	3	US-09-066-028-23	Sequence 23, Appli
5	383	71.1	78	4	US-09-335-325-23	Sequence 23, Appli
6	350	64.9	78	2	US-08-612-788-22	Sequence 22, Appli
7	350	64.9	78	3	US-09-066-028-22	Sequence 22, Appli
8	350	64.9	78	4	US-09-335-325-22	Sequence 22, Appli
9	285	52.9	78	2	US-08-612-788-17	Sequence 17, Appli
10	285	52.9	78	3	US-09-066-028-17	Sequence 17, Appli
11	281	52.9	78	4	US-09-335-325-17	Sequence 17, Appli
12	281	52.1	78	2	US-08-612-788-18	Sequence 19, Appli
13	281	52.1	78	2	US-08-612-788-19	Sequence 19, Appli
14	281	52.1	78	3	US-09-066-028-18	Sequence 18, Appli
15	281	52.1	78	3	US-09-066-028-19	Sequence 18, Appli
16	281	52.1	78	4	US-09-335-325-18	Sequence 18, Appli
17	281	52.1	78	4	US-09-335-325-19	Sequence 19, Appli
18	278	51.6	78	2	US-08-612-788-20	Sequence 20, Appli
19	278	51.6	78	3	US-09-066-028-20	Sequence 20, Appli
20	278	51.6	78	4	US-09-335-325-20	Sequence 20, Appli
21	277	51.4	78	2	US-08-763-528A-4	Sequence 21, Appli
22	273	50.6	78	2	US-08-612-788-21	Sequence 21, Appli
23	273	50.6	78	3	US-09-066-028-21	Sequence 21, Appli
24	273	50.6	78	4	US-09-335-325-21	Sequence 21, Appli
25	251	46.6	90	1	US-08-643-219-4	Sequence 4, Appli
26	251	46.6	90	2	US-09-131-995-4	Sequence 4, Appli
27	46.6	90	2	US-08-832-087B-4	Sequence 4, Appli	

ALIGNMENTS

RESULT 1	US-09-348-953-2	Query Match	75.1%	Score 405;	Best Local Similarity	79.8%	Pred. No. 1 3e-36;
	; Sequence 2, Application US/09348953	Matches 67;	Conservative	Mismatches 11;	Indels 0;	Gaps 0;	
	; Patent No. 6538103						
	; GENERAL INFORMATION:						
	; APPLICANT: JI, Richard Wei-Dong						
	; TITLE OF INVENTION: LYSINE BINDING FRAGMENTS OF ANGIOSTATIN						
	; FILE REFERENCE: DB11Sequences						
	; CURRENT APPLICATION NUMBER: US/09/348,953						
	; PRIORITY FILING DATE: 1999-07-07						
	; PRIOR APPLICATION NUMBER: 60,092,831						
	; NUMBER OF SEQ ID NOS: 8						
	; SOFTWARE: PatentIn Ver. 2.0						
	; SEQ ID NO: 2						
	; LENGTH: 84						
	; TYPE: PRT						
	; ORGANISM: human						
	US-09-348-953-2						

```

; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,788
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05940-0251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..78
; OTHER INFORMATION: /note= "Kringle 4 - Figure 3"
; US-08-763-528A-5

Query Match 71.1%; Score 383; DB 2; Length 78;
Best Local Similarity 79.5%; Pred. No. 2.9e-34;
Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 CYHGDRSYRGSISSTVGRTCQSWSMIPWHQRTPEYNPAGLTYCRNPDSKQPW 67
Db 1 CYHDGDSYRGSISSTTGRKCQSQSSMTPHRHQKTPENYPAGLMNYCRNPDAKGFW 60

QY 68 CYTTDPYRWEYCNLQC 85
Db 61 CFTDPYRWEYCNLKC 78

Query Match 71.1%; Score 383; DB 2; Length 78;
Best Local Similarity 79.5%; Pred. No. 2.9e-34;
Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
RESULT 4
US-09-066-028-23
; Sequence 23, Application US/09066028
; Patent No. 602488
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Anglostatin Fragments and Method of use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Astor
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,028
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/612,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799

; COUNTRY: US
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,528A
; FILING DATE: 12-DEC-1996
; CLASSIFICATION: 530
;
```

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLogy: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: K4

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-335-325-23

Query Match 71.1%; Score 383; DB 4; Length 78;
 Best Local Similarity 79.5%; Pred. No. 2, 9e-4;
 Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0

Query Match 71.1%; Score 383; DB 3; Length 78;
 Best Local Similarity 79.5%; Pred. No. 2, 9e-4;
 Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0

Query Match 71.1%; Score 383; DB 3; Length 78;
 Best Local Similarity 79.5%; Pred. No. 2, 9e-4;
 Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0

Y 8 CYHGDGRSYRGISSTTYGRTQWSMTPHWHORTPNAGLITENYCRNPDGKQPW 67
 Y 8 CYHGDGRSYRGISSTTYGRTQWSMTPHWHORTPNAGLITENYCRNPDGKQPW 67
 b 1 CYHGDQSYRGTSSTTGKQCSWMSMPHRHOKTPNAGLITMNYCRNPDADKGPW 60

RESULT 6
 US-08-612-788-22
 Sequence 22, Application US/08612788
 Patent No. 5837682

GENERAL INFORMATION:
 APPLICANT: Folman, M. Judah
 APPLICANT: Cao, Yihai
 APPLICANT: O'Reilly, Michael
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335.325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE DOCKET NUMBER: 05213-0126

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLogy: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Murine
 IMMEDIATE SOURCE:
 CLONE: K4

US-08-612-788-22

Query Match 64.9%; Score 350; DB 2; Length 78;
 Best Local Similarity 70.5%; Pred. No. 1e-30;
 Matches 55; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 Qy 8 CYHGDGRSYRGSSTTVGRTQCSWSSMIPHWHORTPEYNPNAGLTTENYCRNPDGKOPW 67
 Db 1 CTDGDSYRTSSTTINGKKCQSWAAMFPHRSKTPENFDAGLEMNTCRNPDGKOPW 60

RESULT 8
 US-09-335-325-22
 ; Sequence 22, Application US/09335325
 ; Patent No. 652439
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; O'Reilly, Michael
 ; Cao, Yihai
 ; Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/335,325
 ; FILING DATE: 17-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE: 08/612,788
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 05213-0126
 ; REFERENCE/DOCKET NUMBER: 36,714
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3799
 ; FAX: 404-818-3799
 ; INFORMATION FOR SEQ ID NO: 22:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/612,788
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 05213-0126
 ; REFERENCE/DOCKET NUMBER: 36,714
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3799
 ; FAX: 404-818-3799
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 78 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Murine
 ; IMMEDIATE SOURCE:
 ; CLONE: K4
 US-09-066-028-22

Query Match 64.9%; Score 350; DB 3; Length 78;
 Best Local Similarity 70.5%; Pred. No. 1e-30;
 Matches 55; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 Qy 8 CYHGDGRSYRGSSTTVGRTQCSWSSMIPHWHORTPEYNPNAGLTTENYCRNPDGKOPW 67
 Db 1 CTDGDSYRTSSTTINGKKCQSWAAMFPHRSKTPENFDAGLEMNTCRNPDGKOPW 60

RESULT 8
 US-09-335-325-22
 ; Sequence 22, Application US/09335325
 ; Patent No. 652439
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; O'Reilly, Michael
 ; Cao, Yihai
 ; Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/335,325
 ; FILING DATE: 17-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE: 08/612,788
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05213-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3799
 ; FAX: 404-818-3799
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 ; Query Match 64.9%; Score 350; DB 4; Length 78;
 ; Best Local Similarity 70.5%; Pred. No. 1e-30;
 ; Matches 55; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 Qy 8 CYHGDGRSYRGSSTTVGRTQCSWSSMIPHWHORTPEYNPNAGLTTENYCRNPDGKOPW 67
 Db 1 CTDGDSYRTSSTTINGKKCQSWAAMFPHRSKTPENFDAGLEMNTCRNPDGKOPW 60

RESULT 8
 US-09-335-325-22
 ; Sequence 22, Application US/09335325
 ; Patent No. 652439
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; O'Reilly, Michael
 ; Cao, Yihai
 ; Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/335,325
 ; FILING DATE: 17-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE: 08/612,788
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05213-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3799
 ; FAX: 404-818-3799
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 ; Query Match 64.9%; Score 350; DB 4; Length 78;
 ; Best Local Similarity 70.5%; Pred. No. 1e-30;
 ; Matches 55; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 Qy 8 CYHGDGRSYRGSSTTVGRTQCSWSSMIPHWHORTPEYNPNAGLTTENYCRNPDGKOPW 67
 Db 1 CTDGDSYRTSSTTINGKKCQSWAAMFPHRSKTPENFDAGLEMNTCRNPDGKOPW 60

RESULT 9
 US-08-612-788-17
 ; Sequence 17, Application US/08612788
 ; Patent No. 5837882
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Micheal
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: U.S.
 ; ZIP: 30303-1769
 ; COMPUTER READEABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0., Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE:
 ; PRIORITY APPLICATION DATA:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION NUMBER: 08/612,788
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05213-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-7799
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 78 amino acids
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-7799
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 78 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Murine
 ; IMMEDIATE SOURCE:
 ; CLONE: K3
 ; US-08-612-788-17

Query Match
 Best Local Similarity 59.0%; Pred. No. 1e-23; Length 78;
 Matches 46; Conservative 6; Mismatches 26; Indels 0; Gaps 0;

QY 8 CYHGDGRSYRGISSTVTGRTCQSWSMIPHWHORTPNYPNAGLJENYCRNPDSGKQPW 67
 Db 1 CLKGRENYRGTYSVIVSGKTQRMSEQTPHHRNRPENPCKLNENICRNPDGETAPW 60
 RESULT 11
 US-09-066-028-17
 ; Sequence 17, Application US/09066028
 ; Patent No. 602468
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Micheal
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use

RESULT 10
 US-09-066-028-17
 ; Sequence 17, Application US/09066028
 ; Patent No. 602468
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Micheal
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use

NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READEABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0., version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Marine
 IMMEDIATE SOURCE:
 CLONE: K3
 US-09-066-028-17

Query Match
 Best Local Similarity 59.0%; Pred. No. 1e-23; Length 78;
 Matches 46; Conservative 6; Mismatches 26; Indels 0; Gaps 0;

QY 8 CYHGDGRSYRGISSTVTGRTCQSWSMIPHWHORTPNYPNAGLJENYCRNPDSGKQPW 67
 Db 1 CLKGRENYRGTYSVIVSGKTQRMSEQTPHHRNRPENPCKLNENICRNPDGETAPW 60
 RESULT 11
 US-09-335-328-17
 ; Sequence 17, Application US/09335325
 ; Patent No. 6521439
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; O'Reilly, Micheal
 ; Cao, Yihai
 ; Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: U.S.

ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335,325
 FILING DATE: 17-Jan-1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TOPOLOGY: linear
 HYPOTHETICAL: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: K3
 US-08-612-788-18

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Murine
 IMMEDIATE SOURCE:
 CLONE: K3
 US-09-335-325-17

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 Best Local Similarity 59.0%; Score 285; DB 4; Length 78;
 Matches 46; Conservative 6; Missmatches 26; Indels 0; Gaps 0;
 RESULT 13
 US-08-612-788-19

QY 8 CYHDGDSYRGTISSTVTGRTCSWSSMIPHWHQTPENYNPNAGLTCRNPDSGKQDW 67
 Db 1 CLKGGRGNRYRTSTVSSKTCRWSQEQTPHRHNTPEPNCPKNLBNENCRNPDPGETADW 60

QY 68 CYTDPGYRWTYCNCNTOC 85
 Db 61 CYTDSQRLRWEYCEPSC 78

RESULT 12
 US-08-612-788-18
 Sequence 18, Application US/08612788
 Patent No. 5837682
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 SPARDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rhesus monkey
 IMMEDIATE SOURCE:
 CLONE: K3
 US-08-612-788-19

Query Match 52.1%; Score 281; DB 3; Length 78;
 Best Local Similarity 57.7%; Pred. No. 2.7e-23;
 Matches 45; Conservative 7; Mismatches 26; Indels 0; Gaps 0;

QY 8 CYGDGSYRGISSTTGRICQSSSMAPWHQRTPENPNAGLTENCRNPDGKQFW 67
 Db 1 CLKGTGNGENRGNAYVZSGHTCQHWSAQTPHTHNRTPENPSKNLDENCRNPDGKRAPW 60

Query Match 52.1%; Score 281; DB 3; Length 78;
 Best Local Similarity 57.7%; Pred. No. 2.7e-23;
 Matches 45; Conservative 7; Mismatches 26; Indels 0; Gaps 0;

QY 8 CYGDGSYRGISSTTGRICQSSSMAPWHQRTPENPNAGLTENCRNPDGKQFW 67
 Db 1 CLKGTGNGENRGNAYVZSGHTCQHWSAQTPHTHNRTPENPSKNLDENCRNPDGKRAPW 60

RESULT 14
 Sequence 18, Application US/09066028
 Parent No. 6024688
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Micheal
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1., Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 SPARDEDNESS:
 TOPOLOGY: linear

MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rhesus monkey
 IMMEDIATE SOURCE:

;	CLONE:	K3
	US-09-066-028-19	
Query	Match	Score 281; DB 3; Length 78;
Best Local	Similarity 57.7%; Pred. No. 2.7e-23;	
Matches	45; Conservative 7; Mismatches 26; Indels 0; Gaps 0;	
QY	8 CIEHDGSRYGLISSTVTGTCOSWSSNMIPBHQTRPENPVNAGLTLTENYCNRNPDGSKQPW 67	
Ds	1 CLKGTCENYGRGAATVSGHTCIGWSAQTPATHNRTPENFPCNMIDENYCNRNPDGKAPW 60	
QY	68 CYTDDPVCYRWEWCNLTQC 85	
Db	61 CYTINSQYRWECKPKSC 78	

Search completed: September 29, 2003, 08:23:21
Job time : 31 secs

GenCore version 5.1.6
 Copyright (C) 1993 - 2003 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: September 29, 2003, 08:22:08 ; Search time 63 Seconds
 (without alignments)
 218.555 Million cell updates/sec

Title: US-10-088-548-4
 Perfect score: 539
 Sequence: 1 KSPVYQDCYHGDGRSYRGIS.....DPCVRMEYCNLTQCSETESG 91

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters: 203300

Minimum DB seq length: 0
 Maximum DB seq length: 91

Post-processing: Minimum Match 100%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_AA:
 1: /cgn2_6/podata/1/pubpaas/US07_PUBCOMB.pep:
 2: /cgn2_6/podata/1/pubpaas/PC_T_.pep:
 3: /cgn2_6/podata/1/pubpaas/US06_PUBCOMB.pep:
 4: /cgn2_6/podata/1/pubpaas/US06_PUBCOMB.pep:
 5: /cgn2_6/podata/1/pubpaas/US07_NEW_PUB.pep:
 6: /cgn2_6/podata/1/pubpaas/PCUTS_PUBCOMB.pep:
 7: /cgn2_6/podata/1/pubpaas/US08_NEW_PUB.pep:
 8: /cgn2_6/podata/1/pubpaas/US08_PUBCOMB.pep:
 9: /cgn2_6/podata/1/pubpaas/US09A_PUBCOMB.pep:
 10: /cgn2_6/podata/1/pubpaas/US09A_PUBCOMB.pep:
 11: /cgn2_6/podata/1/pubpaas/US09C_PUBCOMB.pep:
 12: /cgn2_6/podata/1/pubpaas/US09C_NEW_PUB.pep:
 13: /cgn2_6/podata/1/pubpaas/US10A_PUBCOMB.pep:
 14: /cgn2_6/podata/1/pubpaas/US10B_PUBCOMB.pep:
 15: /cgn2_6/podata/1/pubpaas/US10C_PUBCOMB.pep:
 16: /cgn2_6/podata/1/pubpaas/US10_NEW_PUB.pep:
 17: /cgn2_6/podata/1/pubpaas/US60_NEW_PUB.pep:
 18: /cgn2_6/podata/1/pubpaas/US60_PUBCOMB.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	383	71.1	78	9	US-09-753-064-5
2	383	71.1	78	9	US-09-761-120-23
3	383	71.1	78	10	US-09-335-325-23
4	383	71.1	78	12	US-10-267-137-9
5	383	71.1	78	15	US-10-131-241-23
6	350	64.9	78	9	US-09-761-120-22
7	350	64.9	78	10	US-09-335-325-22
8	350	64.9	78	15	US-10-131-241-22
9	285	52.9	78	9	US-09-761-120-17
10	285	52.9	78	10	US-09-335-325-17
11	285	52.9	78	15	US-10-131-241-17
12	281	52.1	78	9	US-09-761-120-19
13	281	52.1	78	10	US-09-335-325-18
14	281	52.1	78	10	US-09-335-325-19
15	281	52.1	78	15	US-10-131-241-18

ALIGNMENTS

Sequence 19, Appl
 Sequence 20, Appl
 Sequence 20, Appl
 Sequence 20, Appl
 Sequence 4, Appl
 Sequence 16, Appl
 Sequence 21, Appl
 Sequence 21, Appl
 Sequence 21, Appl
 Sequence 21, Appl
 Sequence 12, Appl
 Sequence 9, Appl
 Sequence 9, Appl
 Sequence 11, Appl
 Sequence 11, Appl
 Sequence 16, Appl
 Sequence 16, Appl
 Sequence 2, Appl
 Sequence 8, Appl
 Sequence 10, Appl
 Sequence 8, Appl
 Sequence 10, Appl
 Sequence 7, Appl
 Sequence 8, Appl
 Sequence 10, Appl
 Sequence 7, Appl
 Sequence 8, Appl
 Sequence 10, Appl
 Sequence 7, Appl
 Sequence 10, Appl
 Sequence 7, Appl
 Sequence 7, Appl
 Sequence 15, Appl

RESULT 1

US-09-753-064-5

; Sequence 5, Application US/09753064
 ; Patent No. US20010016644A1

GENERAL INFORMATION:

; Cao, Yihai

; FOLKMAN, M. Judah

; TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jones & Askew, LLP

; STREET: 191 Peachtree Street, 37th Floor

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: US

; ZIP: 30303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 12-DEC-1996

; FILING DATE: 29-Dec-2000

; CLASSIFICATION DATA: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/763,528

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren, William L.

; REGISTRATION NUMBER: 36,714

; REFERENCE/DOCKET NUMBER: 05940-0251

; TELECOMMUNICATION INFORMATION:

; TELEFAX: 404-818-3700

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
 /

LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..78
 OTHER INFORMATION: /note= "Kringle 4 - Figure 4 - Figure 3"
 SEQUENCE DESCRIPTION: SEQ ID NO: 5;
 US-09-753-064-5

Query Match 71.1%; Score 383; DB 9; Length 78;
 Best Local Similarity 79.5%; Pred. No. 3.8e-34;
 Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 CYHGDRSRYGSISSTTGRCQSNSSMIPHWTTPENYNAGLTENCRNDSGQPW 67
 Db 1 CYHGDRSRYGTSSTTGTGKKCQSNSSMTPHRHOKTPEYNFNGLTMTCRNPFDADKGFW 60

QY 68 CYTTDPCVREYCNLTQC 85
 Db 61 CFTTDPSVREYCNLKCC 78

RESULT 2
 US-09-751-120-23
 / Sequence 23, Application US/09761120
 / Patent No. US2003020037847A1
 / GENERAL INFORMATION:
 / APPLICANT: Polkman, M. Judah
 / TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
 / FILE REFERENCE: 05940-0151 (4317-25068)
 / CURRENT APPLICATION NUMBER: US/09-7761,120
 / CURRENT FILING DATE: 2001-01-16
 / PRIOR APPLICATION NUMBER: 09/309,821
 / PRIOR FILING DATE: 1999-05-11
 / PRIOR APPLICATION NUMBER: 08/866,735
 / PRIOR FILING DATE: 1997-05-30
 / NUMBER OF SEQ ID NOS: 47
 / SOFTWARE: Patentin version 3.0
 / SEQ ID NO: 23
 / LENGTH: 78
 / TYPE: PPT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc_feature
 / OTHER INFORMATION: Kringle 4
 US-09-751-120-23

Query Match 71.1%; Score 383; DB 9; Length 78;
 Best Local Similarity 79.5%; Pred. No. 3.8e-34;
 Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 CYHGDRSRYGSISSTTGRCQSNSSMIPHWTTPENYNAGLTENCRNDSGQPW 67
 Db 1 CYHGDRSRYGTSSTTGTGKKCQSNSSMTPHRHOKTPEYNFNGLTMTCRNPFDADKGFW 60

QY 68 CYTTDPCVREYCNLTQC 85
 Db 61 CFTTDPSVREYCNLKCC 78

RESULT 4
 US-10-267-137-9
 / Sequence 9, Application US/10067137
 / Publication No. US20030148950A1
 / GENERAL INFORMATION:
 / APPLICANT: Xin, Li
 / APPLICANT: Li, Zai-Ping
 / APPLICANT: Gan, Ren-bao
 / APPLICANT: Zhou, Qing-wei
 / APPLICANT: Xu, Ren
 / TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCYTE GROWTH FACTOR AND USES THEREFOR
 / TITLE OF INVENTION:

RESULT 3
 US-09-335-325-23
 / Sequence 23, Application US/09335325
 / Patent No. US2002016471A1
 / GENERAL INFORMATION:
 / APPLICANT: Folkman, M. Judah

FILE REFERENCE: 524282000100
; CURRENT APPLICATION NUMBER: US/10/267-137
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/328,329
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence alignment of Kringle domains of
; Other Information: Plasminogen and HGF
US-10-267-137-9

Query Match 71.1%; Score 383; DB 12; Length 78;
Best Local Similarity 79.5%; Pred. No. 3.8e-34;
Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 CYHGDSRGSYISSSTVGRTCQSSMTPHQRTPENPNAGLTYCRNPDSKQFW 67
Db 1 CYHGDSRGSYRTGTSSTTGGCQSWSMTPHRHQTKPENPNAGLTYCRNPDAKGPW 60

QY 68 CTTTDPCKVWEYCNLTOC 85
Db 61 CTTTDPCKVWEYCNLKKC 78

RESULT 5
US-10-131-241-23
; Publication No. US2003001279A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; FORTIER, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
; FILE REFERENCE: 05213-0344 43170-21565
; CURRENT APPLICATION NUMBER: US/10/131,241
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-23

Query Match 71.1%; Score 383; DB 15; Length 78;
Best Local Similarity 79.5%; Pred. No. 3.8e-34;
Matches 62; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 CYHGDSRGSYISSSTVGRTCQSSMTPHQRTPENPNAGLTYCRNPDSKQFW 67
Db 1 CYHGDSRGSYRTGTSSTTGGCQSWSMTPHRHQTKPENPNAGLTYCRNPDAKGPW 60

QY 68 CTTTDPCKVWEYCNLTOC 85
Db 61 CTTTDPCKVWEYCNLKKC 78

RESULT 6
US-09-761-120-22
; Sequence 22, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:

```

; LENGTH: 78 amino acids
; TYPE: amino acid
; STRANDDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Murine
; IMMEDIATE SOURCE:
; CLONE: K4
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-09-335-325-22

Query Match 64.9%; Score 350; DB 10; Length 78;
Best Local Similarity 70.5%; Pred. No. 1.4e-30;
Matches 55; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
; SEQ ID NO: 17
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-09-761-120-17

QY 8 CYHGDRSYRGISSTTVGRTCSWSSMIPHWHORTPEYNYCRNPDSGKOPW 67
Db 1 CRYGDGSYRGTSSITGKKCOSWAAMFPHRSKTPENFDAGLENYCRNPDGKCPW 60
; SEQ ID NO: 17
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-09-761-120-17

Qy 8 CYHGDRSYRGISSTTVGRTCSWSSMIPHWHORTPEYNYCRNPDSGKOPW 67
Db 1 CRYGDGSYRGTSSITGKKCOSWAAMFPHRSKTPENFDAGLENYCRNPDGKCPW 60
; SEQ ID NO: 17
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-09-761-120-17

Qy 8 CYHGDRSYRGISSTTVGRTCSWSSMIPHWHORTPEYNYCRNPDSGKOPW 67
Db 1 CRYGDGSYRGTSSITGKKCOSWAAMFPHRSKTPENFDAGLENYCRNPDGKCPW 60
; SEQ ID NO: 17
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-09-761-120-17

QY 68 CYTIDPCYRWEYCNLTC 85
Db 61 CYTIDPSVRWEYCNLKC 78
; SEQ ID NO: 22
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-10-131-241-22

; Sequence 22, Application US/10131241
; Application No. US003001292A1
; GENERAL INFORMATION:
; APPLICANT: Holiday, John W.
; ATTORNEY/AGENT INFORMATION:
; FORTIER, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
; FILE REFERENCE: 05213-0344 43170-27165
; CURRENT APPLICATION NUMBER: US10/131241
; CURRENT FILING DATE: 2003-07-22
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-05-22
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: US 09/086,586
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 22
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-10-131-241-22

Query Match 64.9%; Score 350; DB 15; Length 78;
Best Local Similarity 70.5%; Pred. No. 1.4e-30;
Matches 55; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
; SEQ ID NO: 22
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-10-131-241-22

QY 8 CYHGDRSYRGISSTTVGRTCSWSSMIPHWHORTPEYNYCRNPDSGKOPW 67
Db 1 CRYGDGSYRGTSSITGKKCOSWAAMFPHRSKTPENFDAGLENYCRNPDGKCPW 60
; SEQ ID NO: 22
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-10-131-241-22

QY 68 CYTIDPCYRWEYCNLTC 85
Db 61 CYTIDPSVRWEYCNLKC 78
; SEQ ID NO: 22
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Murinae sp.
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 3
US-10-131-241-22

; Sequence 17, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; ATTORNEY/AGENT INFORMATION:
; WARREN, William L.
; REGISTRATION NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; 
```


Wed Oct 1 15:58:36 2003

us-10-088-548-4.sep29.rappb

Page 6

STRANDEDNESS: <Unknown>
TOPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K3
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-335-325-18
Query Match 52.1%; Score 281; DB 10; Length 78;
Best Local Similarity 56.4%; Pred. No. 4e-23;
Matches 44; Conservative 10; Mismatches 24; Indels 0; Gaps 0;
Qy 8 CYHGDRGSRGSSSTVGRTCQSWSMIPHWHORTPENPNAGLITENCRNPDGKOPW 67
Db 1 CLKSTGENYRGDVATVSGHTCWSACTPHNTPENPCRNLDENCRNPDPGEKFW 60
RESULT 15
US-10-131-241-18
Qy 68 CYTTDPCVRWEYCNLTC 85
Db 61 CHTNSQVRWEYCIPSC 78
RESULT 14
US-09-335-325-19
Sequence 19, Application US/09335325
; Patent No. US2002016471A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Michael
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Aniostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1768
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335.325
FILING DATE: 17-Jun-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

Search completed: September 29, 2003, 08:32:03
Job time : 64 secs

GenCore version 5.1.6						
Copyright (C) 1993 - 2003 Compugen Ltd.						
MM protein - protein search, using sw model						
run on:	September 29, 2003, 08:12:27	Search time 40 Seconds				
	(without alignments)					
	218.784 Million cell updates/sec					
title:	US-10-088-548-4					
perfect score:	539					
sequence:	KSPVYQDCYHGDRSRYGIS.....					
scoring table:	BLOSUM62					
Gapext:	10.0					
gapext score:	0.5					
searched:	283308 seqs, 96168652 residues					
total number of hits satisfying chosen parameters:	32085					
minimum DB seq length:	0					
maximum DB seq length:	91					
post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
database :	PIR_7616.*					
	1: pi1;*					
	2: pi2;*					
	3: pi3;*					
	4: pi4;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
result No.	Score	Query Match	Length	DB ID	Description	
1	329	61.0	89	A0140	plasmin (EC 3.4.2.1)	
2	66	12.2	86	S21651	Ig heavy chain V	
3	57	10.7	77	T14395	protease inhibitor	
4	55	10.3	86	A31910	muscarinic toxin	
5	55	10.3	88	S16161	BUT14 protein - b	
6	55	10.2	86	S20459	Ig kappa chain V	
7	55	10.2	86	S29587	Ig kappa chain V	
8	54	10.0	57	T2NJB	short toxin CM-11	
9	52.5	9.7	67	S24216	Ig kappa chain -	
10	51.5	9.6	55	D98636	unknown protein,	
11	51	9.5	88	G69136	ribosomal protein	
12	50	9.3	72	D5557	hypothetical protein	
13	50	9.3	76	IHER2	high potential hit	
14	49.5	9.2	82	JCS892	cobrotoxin b - CII	
15	49.5	9.2	84	PS0142	replication associa-	
16	49	9.1	72	Q3ECS	hypothetical 8K F	
17	49	9.1	81	IPDK	insulin precursor	
18	48.5	9.0	72	NDEP1V	long neurotoxin I	
19	48.5	9.0	77	S30578	protease inhibitor	
20	48.5	9.0	84	E88209	protein F22G5.16	
21	48.5	9.0	86	S78488	Ig kappa chain V	
22	48.5	9.0	89	P0129	class II histocom-	
23	48.5	9.0	89	I65555	MHC class II histi-	
24	48	8.9	87	B60549	kappa-3 neurotoxin	
25	48	8.8	89	S38704	MHC class II histi-	
26	47.5	8.8	55	S34330	sox protein - lec-	
27	47.5	8.8	62	NINJ3M	short neurotoxin	
28	47.5	8.8	77	B84433	Ig kappa chain V	
29	47.5	8.8	86	S34086	protease inhibitor	

0	47.5	8.8	87	2	S34064
1	47.5	8.8	87	2	S34083
2	47.5	8.8	88	2	S21328
3	47.5	8.8	88	2	S21522
4	47	8.7	55	2	E58392
5	47	8.7	62	2	G25366
6	47	8.7	66	2	PQ0442
7	47	8.7	66	2	PQ0440
8	47	8.7	70	2	T32446
9	47	8.7	73	2	AD1043
0	47	8.7	87	2	S16342
1	47	8.7	87	2	S16341
2	46.5	8.6	87	2	C84433
3	46.5	8.6	81	2	A41441
4	46	8.5	61	1	NIR12
5	46	8.5	76	2	T34487

ALIGNMENTS

RESULT 1

A60140 plasmin (EC 3.4.21.7) precursor - chicken (fragment)
 NyAlternate names: plasminogen
 C:Species: Gallus gallus (chicken)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
 C:Accession: A60140
 R:Biophys. Acta 832, 326-339, 1985
 A:Title: The kringle 4 domain of chicken plasminogen.
 A:Reference: A60140; PMID:8607796; PMID:4074753
 A:Accession: A60140
 A:Molecule type: protein
 A:Residues: 1-89 <GYE>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homologous proteins
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinas
 F:6-83/Domain: kringle homology <KRIG>
 F:6-83/27-56:55-78/Disulfide bonds: #status predicted
 F:39/Binding site: carbohydrate (asn) (covalent) #status experimental

	Query Match	Score	DB 2;	Length	89;
Best Local Similarity	61.0%	Pred.	No.	2e-25;	
Matches	50;	Mismatches	16;	Indels	0;
Gaps	0;				

Qy 6 QDCFEGDGSYRATISSTETVTCGSSSMIPWHQRTPEVNPNGLTENYCRAFPDSQQ 65
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 4 EECGTQNGSYRGTASSTITTKKCOANNSMSPHRKNTKTESHPNADLQRNYCRNPADRS 63

Qy 66 PWCYTTDPVCWRYCNLTOCSE 87
 |||:|||:|||:|||:|||:|||:
 Db 64 PWCYTTDPVSRYCNLKRCSD 85

RESULT 2

S20651 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Accession: S20651; #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S20651; #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 R:Liosman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
 submitted to the EMBL Data Library, February 1992
 A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice 1
 A:Reference number: S20639
 A:Accession: S20651
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-86 <S>>
 A:Cross-references: EMBL:X65007; NID:652647; PIDN:CAA46140; PMID:952648; EMBL:X65014
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin

Best Local Similarity 25.4%; Pred. No. 10; Mismatches 22; Indels 24; Gaps 2;
 Matches 18; Conservative 7; N mismatches 2; N indels 2; N gaps 2;
 A; Molecule type: protein
 A; Residues: 22-27 29-86 <SGC>
 C; Superfamily: snake toxin
 C; Keywords: toxin; venom
 F: 1-21.Domain: signal sequence # status predicted <SIG>
 F: 22-86.Product: muscarinic toxin 2 #status experimental <MAT>

Query Match 10.3%; Score 55.5; DB 2; Length 86;
 Best Local Similarity 28.8%; Pred. No. 1.1e+02; Mismatches 31; Indels 1; Gaps 1;
 Matches 15; Conservative 5; N mismatches 31; N indels 1; N gaps 1;

Qy 24 VYGRTCQNSSM-IPHEWQRTPEVNPAGLITENYCRNPDSKGKOPNCYTIDPC 74
 Db 33 VTEDQAPCONVCEKRVHVVTPKNDITKGAACTPKVDNNP1RCGGTDDKC 84

RESULT 3

T14395
 proteinase inhibitor II - turnip
 C;Species: Brassica rapa (turnip)
 C;Date: 20-Sep-1999 #sequence_revision 20-Jun-2000
 C;Accession: T14395
 R;Kim, J.B.; Kim, H.U.; Yun, C.H.; Park, B.S.; Cho, W.S.; Ryu, J.C.; Chung, T.Y.
 submitted to the EMBL Data Library, March 1996
 A;Description: Nucleotide sequences of protease inhibitor II in chinese cabbage.
 A;Reference number: Z18029
 A;Accession: T14395
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-77 <Kim>
 A;Cross-references: EMBL:L1937; NID:91209257; PID:91209258
 A;Experimental source: unopened flower bud
 A;Superfamily: gamma-thionin

Query Match 10.7%; Score 57.5; DB 2; Length 77;
 Best Local Similarity 31.7%; Pred. No. 63; Mismatches 25; Indels 13; Gaps 3;
 Matches 20; Conservative 5; N mismatches 25; N indels 13; N gaps 3;
 A; Molecule type: mRNA
 A; Status: preliminary
 A; Residues: 1-88 <DUN>

Query Match 10.3%; Score 55.5; DB 2; Length 88;
 Best Local Similarity 29.4%; Pred. No. 1.1e+02;
 Matches 20; Conservative 4; Mismatches 25; Indels 19; Gaps 4;
 A; Molecule type: mRNA
 A; Status: preliminary
 A; Residues: 1-88 <DUN>

Qy 18 GISSTVTGRTQCSWSSMIPHWHQRTPEVNPAGLITENYCRNPD----SGKOPNCYT 71
 Db 22 GRGPVTEARTCESKS---HRFKCTCVSSTNCG--NVCHNEGRGGKCRGFVRVCYT 74
 Qy 72 DPC 74
 Db 75 RHC 77

RESULT 4

A37910
 muscarinic toxin 2 precursor - eastern green mamba
 N;Alternative names: MTX2
 C;Species: Dendroaspis angusticeps (eastern green mamba)
 C;Accession: A37910; A37911; S66418
 R;Ducanell, F.; Rowan, E.G.; Cassar, E.; Harvey, A.L.; Menez, A.; Boulain, J.C.,
 Toxicon 29, 516-520, 1991
 A;Title: Amino acid sequence of a muscarinic toxin deduced from the cDNA nucleotide sequ
 A;Reference number: A37910; MUID:91320365; PMID:1862525
 A;Accession: A37910
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-86 <DUC>
 A;Cross-references: GB:X52292; NID:962765; PID:CAA36541.1; PID:g62766
 R;Carlsson, E.; Risinger, C.; Jolkonen, M.; Wernstedt, C.; Adén, A.,
 Toxicon 29, 521-526, 1991
 A;Title: Amino acid sequence of a snake venom toxin that binds to the muscarinic acetyl
 A;Reference number: A37911; MUID:91320366; PMID:1862525
 A;Accession: A37911
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 'K' 23-86 <RAR>
 R;Segalas, I.; Thai, R.; Menez, R.; Vitta, C.,
 PEBS Lett. 371, 171-175, 1995
 A;Title: A particularly labile Asp-Pro bond in the green mamba muscarinic toxin MTX2. Ef
 A;Reference number: S66418; MUID:95402203; PMID:7672121
 A;Accession: S66418
 A;Status: preliminary

Query Match 10.2%; Score 55; DB 2; Length 86;
 Best Local Similarity 28.6%; Pred. No. 1.1e+02;
 Matches 14; Conservative 4; Mismatches 15; Indels 16; Gaps 1;

Qy 23 TYGRTCQNSSMIPHWHQRTPEVNPAGLITENYCRNPDSKGKOPNCYT 71
 Db 4 TTICSVSSISSSNLHWQKSETSP-----KPVYGT 36

RESULT 7

S29587

Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1995
 C:Accession: S29587; S29586
 R:Kavalier, J.
 Submitted to the EMBL Data Library, April 1991
 A:Reference number: S29587
 A:Status: Preliminary
 A: Molecule type: mRNA
 A:Residues: 1-86 <RAV>
 A:Cross-references: EMBL:X59090; NID:952219; PIDN:CAA41816.1; PID:952220; EMBL:X55089; N
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 10.28; Score 55; DB 2; Length 86;
 Best Local Similarity 28.6%; Pred. No. 1.2e+02;
 Matches 14; Conservative 4; Mismatches 15; Indels 16; Gaps 1;
 QY 23 TVTGTTCOSWSSMIPWHQRTPEVNPAGLTENYCRNPDSGKOPWCYT 71
 DB 4 TITCSVSSSISSNNLHWYQQKSETSP-----KEWIGT 36

RESULT 8

T2NBE short toxin CM-1b - ringhals
 C:Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
 C:Accession: A01673
 C:Sequence: 31-Jul-1980 #sequence_revision 31-Jul-1980 #text_change 23-Aug-1996
 R:Toubert, F.J.; Maljaard, N.
 Toxicin 18, 191-198, 1980

A:Title: The complete primary structure of toxin CM-1b from Hemachatus (ring
 A:Reference number: A01673; PMID:80236678; PMID:7394807
 A:Accession: A01673
 A:Molecule type: protein
 A:Residues: 1-57 <IOU>
 C:Superfamily: snake toxin
 C:Keywords: toxin; venom
 F;3-19 12-37,40-49,50-55/disulfide bonds: #status predicted

Query Match 10.0%; Score 54; DB 1; Length 57;
 Best Local Similarity 32.7%; Pred. No. 1e+02;
 Matches 17; Conservative 7; Mismatches 16; Indels 12; Gaps 4;
 QY 28 TCQSSSMIPWHQRTPEVNPAGLTENYCRNPDSGKOPWCYT DPC 74
 DB 11 TCQEQKFC--YSDTMTFFNPVYLSGCT--FCRTDESER--CCTIDRC 55

RESULT 9

S24216 Ig kappa chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Accession: S24216
 R:Shimizu, T.; Iwazato, T.; Yamagishi, H.
 J. Exp. Med. 173, 1065-1072, 1991
 A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular excis
 A:Reference number: S24214; PMID:91217618; PMID:1902500
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-67 <HTI>

A:Cross-references: EMBL:X58221; NID:953719; PIDN:CAA41185.1; PID:9303196
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 9.7%; Score 52.5; DB 2; Length 67;
 Best Local Similarity 34.8%; Pred. No. 1.7e+02;
 Matches 16; Conservative 2; Mismatches 13; Indels 15; Gaps 3;
 QY 11 GDGRSYRGISSTTVTGRGTCQSWSMIPWHQRTPEVNPAGLTENYCRNPDSG 45

Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1995
 C:Accession: S29587; S29586
 R:Kavalier, J.
 Submitted to the EMBL Data Library, April 1991
 A:Reference number: S29587
 A:Status: Preliminary
 A: Molecule type: mRNA
 A:Residues: 1-86 <RAV>
 A:Cross-references: EMBL:X59090; NID:952219; PIDN:CAA41816.1; PID:952220; EMBL:X55089; N
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 10.28; Score 55; DB 2; Length 86;
 Best Local Similarity 28.6%; Pred. No. 1.2e+02;
 Matches 14; Conservative 4; Mismatches 15; Indels 16; Gaps 1;
 QY 23 TVTGTTCOSWSSMIPWHQRTPEVNPAGLTENYCRNPDSGKOPWCYT 71
 DB 4 TITCSVSSSISSNNLHWYQQKSETSP-----KEWIGT 36

RESULT 10

D96636 unknown protein, 87272-87105 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Accession: D96636
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alm
 Chan, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 anser, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzi,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
 ker, M.; Wu, D.; Yiu, G.; Fraser, C.M.; Ventur, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; PMID:21016719; PMID:11130712
 A:Accession: D96636
 A: Molecule type: DNA
 A:Residues: 1-55 <STD>
 A:Cross-references: GB:AE005173; NID:96751695; PIDN:AAF27678.1; GSPDB:GN00141
 C:Genetics:

Query Match 9.6%; Score 51.5; DB 2; Length 55;
 Best Local Similarity 26.6%; Pred. No. 1.8e+02;
 Matches 17; Conservative 7; Mismatches 15; Indels 25; Gaps 3;
 A:Gene: T7P1.20
 A:Map position: 1
 C:Superfamily: gamma-thionin

RESULT 11

QY 23 TYTGRTCQSSSMIPWHQRTPEVNPAGLTENYCRNPDSGKOPWCYT 70
 Db 5 TYEARCTETSSNLF-----NGPQLSSSNANCANVCHNEGFSDDGDR----GFRRRCDC 51

QY 71 TDPC 74
 Db 52 TREC 55

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge,
 Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Tjwani,
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noeiling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: f
 A:Reference number: A69000; PMID:9803754; PMID:9371463
 A:Accession: G69136
 C:Species: Methanobacterium thermoautotrophicum
 C:Accession: G69136
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge,
 Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Tjwani,
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noeiling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: f
 A:Reference number: A69000; PMID:9803754; PMID:9371463
 A:Accession: G69136
 C:Species: eukaryotic ribosomal protein L34; prokaryotic ribosomal protein L
 C:Accession: G69136
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge,
 Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Tjwani,
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noeiling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: f
 A:Reference number: A69000; PMID:9803754; PMID:9371463
 A:Accession: G69136
 C:Species: rat ribosomal Protein L34
 C:Accession: G69136
 A:Molecule type: DNA
 A:Residues: 1-88 <MTD>
 A:Cross-references: GB:AE000796; GB:AE000666; NID:92621057; PIDN:AAB84538.1; PID:926
 A:Experimental source: strain Delta H
 A:Gene: MTB29
 C:Genetics:

Query Match 9.5%; Score 51; DB 2; Length 88;
 Best Local Similarity 31.0%; Pred. No. 3.1e+02;
 Matches 15; Conservative 6; Mismatches 17; Indels 12; Gaps 2;
 QY 14 RSYGRGSISSTVTGRGTCQSWSMIPWHQRTPEVNPAGLTENYCRNPDSG 63

9 RSYKRIFKKTPGGRT-----VTHYRRKKPSKHKVAG-----CGKPLHG 46

Result No.	Score	Query	Match Length	DB ID	Description
1	55.5	10.3	86	1 TXM2_DENAN	P18328 dendroaspis hordeum vul
2	55.5	10.3	88	1 CR14_HORVU	P26154 hordeum vul
3	54	10.0	57	1 TXWB_HEMHA	P01402 hemachatus pseudonaja
4	54	10.0	79	1 NXS6_SETE	P02617 methanobact
5	51	9.5	88	1 RIL34_METTH	026137 methanobact
6	50	9.3	76	1 HP12_FCTHA	P04169 ectobiohorho pseudocellulose receptor.
7	49.5	9.2	82	1 CBTB_RAJAT	P80558 naja attra (escherichia)
8	49	9.1	72	1 YBDZ_BCOLI	P18193 anaerobacter
9	49	9.1	81	1 INS_ANAPL	P01333 anaerobacter plautii
10	48.5	9.0	72	1 NXIL_DENV1	P01394 dendroaspis
11	48.5	9.0	77	1 THG1_BRATH	Q39482 arabidopsis
12	48	8.9	87	1 NXIL_BUNMU	P18177 bunopus mu
13	47.5	8.8	62	1 NXS3_NAJMO	P01432 naja mossambicus
14	47.5	8.8	77	1 THG2_BRATH	Q41914 arabidopsis latimeriae
15	47	8.7	55	1 APP8_PATCH	O03168 laticauda c
16	47	8.7	62	1 NYS2_JLATLA	P01059 laticauda laticauda
17	46.5	8.6	60	1 TX48_DENJA	P25683 dendroaspis
18	46.5	8.6	77	1 THG3_BRATH	Q9yzl7 arabidopsis
19	46	8.5	80	1 TX3A_PHONI	P81793 phoneutria boliviensis
20	46	8.5	49	1 CBIE_TISAL	P1859 viscum albus
21	46	8.5	63	1 CXH_HEMHA	P24778 hemachatus
22	46	8.5	63	1 NXS2_HEMHA	P01195 dendroaspis
23	45.5	8.4	73	1 NXIL_DENV1	P01429 naja haje a
24	45	8.3	61	1 NXSL_NAJWA	P10508 bungarus fasciatus
25	45	8.3	64	1 NXSL_BUNFA	Q97743 sulfobulus
26	45	8.3	70	1 R37A_SULSO	P00292 pseudonaja
27	45	8.3	79	1 NXS1_PPEPE	Q9yhy0 naja attra (
28	44.5	8.3	61	1 CBIV_NAJAT	P0754 anser anser
29	44	8.2	51	1 INS_ANSAN	P25675 naja haje h
30	44	8.2	61	1 NXS2_NAJHH	P37359 bos taurus
31	44	8.2	68	1 MT3_BOVIN	Q02316 corynebacterium
32	44	8.2	76	1 NIKM_BOVIN	Q8ns15
33	44	8.2	78	1 RL28_CORG1	

Scoring table: Biosum62 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 11738

Minimum DB seq length: 0

Maximum DB seq length: 91

Post-processing: Minimum Match 100%

Database : SwissProt_41::

Perfect score: 539

Sequence: US-10-088-548-4
1 KSPVYQDCYHGDRSYRGIS.....DPCVREYNLTQCSETESG 91

ALIGNMENTS

RESULT 1	TXM2_DENAN	STANDARD	PRT;	86 AA.
ID	TXM2_DENAN			
AC	P18328;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DB	Muscarinic toxin 2 precursor.			
OS	Dendroaspis angusticeps (Eastern green mamba).			
OC	Echis carinatus; Chordata; Craniata; Vertebrata;			
OC	Lepidosauria; Squamata; Scelopriidae; Serpentes; Colubroidea;			
OC	Elapidae; Elapinae; Dendroaspis.			
OX	NCBI_TAXID=8618;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Venom gland.			
RX	MEMLINE=91320365; Published=1862324;			
RA	Ducaneil F., Rowan E.G., Cassar E., Harvey A.L., Menez A., Boulaire J.-C.			
RT	"Amino acid sequence of a muscarinic toxin deduced from the cDNA."			
RT	nucleotide sequence."			
RL	Toxicon 29:516-520(1991).			
RN	[2]			
RP	SEQUENCE OF 22-86.			
RC	TISSUE-Venom;			
RX	MEMLINE=91320366; PubMed=1862525;			
RA	Karlsson E., Röslinder C., Jolkhon M., Wernstedt C., Adem A.;			
RT	"Amino acid sequence of a snake venom toxin that binds to the muscarinic acetylcholine receptor."			
RL	Toxicon 29:521-526(1991).			
CC	-!- FUNCTION: BINDS TO THE MUSCARINIC ACETYLCHOLINE RECEPTOR.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Expressed by the venom gland.			
CC	-!- SIMILARITY: Belongs to the snake toxin family.			
CC	[22-86]			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/EMBL/ or send an email to license@isb-sib.ch).			
CC	PIR: A37910; A37910.			
CC	HSSE: P01387; 1NTN.			
DR	InterPro: IPR00572; Cytotoxin.			
DR	InterPro: IPR003571; Snake_toxin.			
DR	Pfam: PF00087; toxin_1.			
DR	PR00282; CYTOTOXIN.			
DR	PRODOM: PD000206; SNAKE_TOXIN_1.			
DR	PROSITE: PS00277; SNAKE_TOXIN_1.			
DR	KW Toxin; Neurotoxin; Signal.			
FT	SIGNAL	1	21	
FT	CHAIN	22	86	MUSCARINIC_TOXIN_2.
FT	DISULFID	24	45	BY SIMILARITY.

FT	DISULFID	38	63	BY SIMILARITY.	
FT	DISULFID	67	78	BY SIMILARITY.	
FT	DISULFID	79	84	BY SIMILARITY.	
SQ	SEQUENCE	86 AA;	9375 MW;	6F062C970074D53 CRC64;	
Query Match	24 VIGRTCOSWSSM-TIPWHWORTPENYPAQLTENYCRNPDSGKQPWCYTTEPC 74	Score 55.5; DB 1; Length 86;			
Best Local Similarity	28.8%; Pred. No. 27;				
Matches 15; Conservative 5; Mismatches 31; Indels 1; Gaps 1;					
RESULT 2					
CRI14_HORVU	STANDARD	PRT;	88 AA.		
ID CRI14_HORVU	P26154;	(Rel. 22, Created)			
AC P26154;	DT 01-MAY-1992	(Rel. 22, Last sequence update)			
DT 28-FEB-2003	(Rel. 41, Last annotation update)				
DE Cold-regulated protein BLT14.					
GN BLT14.					
OS Hordeum vulgare (Barley).	Streptophytina: Embryophyta: Tracheophyta;				
OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;					
OC Spermatophytina;					
OC Triticeae; Hordeum.					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=cy. Igri; TISSUE=Shoot meristem;					
RA Dunn M.A., Hughes M.A., Pearce R.S., Jack P.L.;					
RT Molecular characterization of a barley gene induced by cold treatment.";					
RT J. Exp. Bot. 41:1405-1413(1990).					
CC -!- INDUCTION: By cold stress.					
CC -!- MISCELLANEOUS: CONTAINS SEVERAL ARGININE RESIDUES IN CLOSE PROXIMITY WHICH MAY BE INVOLVED IN PROTEIN RNA INTERACTIONS.					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC DR EMBL_X57554; CDA40779.1; -.					
CC DR; S16161; S16161.					
KW RNA-binding.					
FT DOMAIN	32	41	ARG-RICH		
SQ SEQUENCE	88 AA;	9796 MW;	C15ED831EPBD4000 CRC64;		
Query Match	10.3%; Pred. No. 28;	Score 55.5; DB 1; Length 88;			
Best Local Similarity	29.4%; Pred. No. 28;				
Matches 20; Conservative 4; Mismatches 25; Indels 19; Gaps 4;					
RESULT 3					
TAWB_HEMHA	STANDARD	PRT;	57 AA.		
ID TAWB_HEMHA	AC P01402;	(Rel. 01, Created)			
DB 21-JUL-1986	(Rel. 01, Last sequence update)				
QY 13 GRSYRGISSTTYTGRCNSKSMIPPHQTPENYPAQLTENYCRNP---DSSGKQPMC 68					
QY 22 GREEGCSDTRC---RCQRW----RRRLQGFGLAAAGGNNRYRNKHYRPAGGDPW- 69					
QY 69 YTTDECYR 76					
DB 70 -->PACYR 74					
SEQUENCE FROM N.A., AND IDENTIFICATION OF INTRONS					
RC TISSUE=Venom gland;					
RX MEDLINE=20279909; PubMed=10818230;					
RA Gong N.L., Arumugam A., Jayaseelan K.;					
RT Molecular cloning, characterization and evolution of the genes encoding a new group of short-chain neurotoxins from <i>Pseudonaja textilis</i> : cDNA cloning, expression and protein characterization.";					
RT Eur. J. Biochem. 265:982-989(1999).					
RL [2]					
RP SEQUENCE FROM N.A., AND IDENTIFICATION OF INTRONS					
RC TISSUE=Venom gland;					
RX MEDLINE=20279909; PubMed=10818230;					
RA Gong N.L., Arumugam A., Jayaseelan K.;					
RT Molecular cloning, characterization and evolution of the genes encoding a new group of short-chain alpha-neurotoxins in an Australian elapid, <i>Pseudonaja textilis</i> .";					
RT FEBS Lett. 473:303-310(2000).					
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic acetylcholine receptors (nAChR) (By similarity).					

ID	INS_ANAPL	STANDARD;	PRP;	81 AA.	
AC	P0133;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Insulin precursor.				
GN	INS.				
OS	Bukaryota; Metazoa; Chordata; Craniaria; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.				
OX	NCBI_TaxID=839;				
RN	[1]				
RP	SEQUENCE OF 1-30 AND 61-81.				
RA	Markussen J.; Sundby F.; PubMed=4763354;				
RA	"Duck insulin: isolation, crystallization and amino acid sequence.";				
RT	"Isolation and amino-acid sequence of the C-peptide of duck insulin."				
RT	"Insulin."				
RL	Int. J. Biochem. 34:401-408(1973).				
CC	- - FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.				
CC	- - SUBUNIT: HETERO-DIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.				
CC	- - SUBCELLULAR LOCATION: Secreted.				
CC	- - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.				
CC	- - CAUTION: X's AT POSITIONS 31-32 AND 59-60 REPRESENT PAIRED BASIC RESIDUES ASSUMED BY HOMOLOGY TO BE PRESENT IN THE PRECURSOR MOLECULE.				
DR	PIR; A01600; IPDK.				
DR	HSPB; P01308; IHS.				
DR	InterPro; IPR004825; Ins/IGF/relax.				
DR	Pfam; PF00044; Insulin; 1.				
DR	PS00262; PS00262; INSULIN; 1.				
KW	Insulin family; Hormone; Glucose metabolism.				
FT	CHAIN 1 30	INSULIN B CHAIN.			
FT	PROPEP 33	C PEPTIDE.			
FT	CHAIN 61	INSULIN A CHAIN.			
FT	DISULFID 7	INTERCHAIN.			
FT	DISULFID 19	INTERCHAIN.			
FT	DISULFID 66	INTERCHAIN.			
SQ	SEQUENCE 81 AA;	9100 MW;	6EA8A271F099DA91 CRC64;		
Query Match	9.1%	Score 49;	DB 1;	Length 81;	
Best Local Similarity	30.4%	Pred. No. 1.2e+02;			
Matches	14;	Conservative	3;	Mismatches 15;	Gaps 3;
QY	36 IPHWHQRTPNAGTENYCRNPDGKQPCYTDPCVRWEYN 81				
DB	50 LPFQH---EEQXQGIVQECNCSC---LIQE-----NVCN 81				
RESULT 10					
ID	NXL1_DENV1	STANDARD;	PRP;	72 AA.	
AC	P01394;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
OS	Dendroaspis viridis (Neurotoxin 4.7/4.9.3).				
CC	Eukaryota; Metazoa; Chordata; Craniaria; Vertebrata; Euteleostomi;				
CC	Squamata; Scleroglossa; Serpentes; Colubroidea;				
CC	Elapidae; Elapinae; Dendroaspis.				
OX	NCBI_TaxID=8621;				
RN					
SEQUENCE FROM N.A.					
RC	SEQUENCE FROM N.A.				
RC	STRAIN=cv. C24; TISSUE=flower buds;				
RC	SPERMATOPHYTA; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
RC	Oeocarpales II; Brassicales; Brassicaceae; Arabidopsis;				
RC	Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.				
[2]					
SEQUENCE FROM N.A.					
RC	SEQUENCE FROM N.A.				
RC	STRAIN=cv. Columbia;				
RC	MEDLINE=20083487; PubMed=10617197;				
RA	Lin X., Kaul S., Rounseley S.D., Shear T.P., Benito M.-I., Town C.D.,				
RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,				
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,				
RA	Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umeyam L.,				
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,				
RA	Goodman H.M., Somerville C.R., Copenhafer G.P., Pruss D.,				
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,				
RA	Venter J.C.;				

RT "Sequence and analysis of chromosome 2 of the Plant Arabidopsis thaliana.";
 RT Nature 402;761-768(1999).
 RN [3].

RP SEQUENCE OF 1-75 TISSUE=Flower buds;

RC STRATN=cv_C24; Thomas F., Yu D.Y.;

RA Machie R., Quigley F.;

RA Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

CC -1- SUBCELLULAR LOCATION: Secreted (Potential).

CC -1- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license@lsb-sib.ch (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

DR EMBL; X69139; CAA8892.1; -.

DR EMBL; Z18455; CAA79189.1; -.

DR PIR; S30578; S30578.

DR HSSP; P20230; IGP.

DR InterPro; IPR002118; Gamma-thionin.

DR InterPro; IPR003614; Knot1.

DR Pfam; PF000304; Gamma-thionin; 1.

DR PRODOM; PD00294; G_purothionin; 1.

DR SMART; SM00505; Knot1; 1.

DR PROSITE; PS00340; GAMMA-THIONIN; 1.

KW Plant defense; Signal; Multigene family; Signal.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 77 GAMMA-THIONIN HOMOLOG AT2G02100.

FT DISULFID 33 77 BY SIMILARITY.

FT DISULFID 44 64 BY SIMILARITY.

FT DISULFID 50 71 BY SIMILARITY.

FT DISULFID 54 73 BY SIMILARITY.

SQ SEQUENCE 77 AA:- 8524 MW; EC04E60C3610965 CRC64;

Query Match 9.0% Score 48.5; DB 1; Length 77;

Best Local Similarity 28.6%; Pred. No. 1.3e+02;

Matches 18; Conservative 6; Mismatches 26; Indels 13; Gaps 3;

QY 18 GISSSTVTGRTCOSWSSMIPWHCPENPNAGLTENCRNPD---SGKOPWCYT 71

DB 22 GMGPTVEARTCQS ---HRFKGTCVVASNCN--NVCHNEGTVGGNCRGFRRCFT 74

QY 72 DPC 74

Db 75 RHC 77

RESULT 12

NXL3_BUNMU ID NXL3_BUNMU STANDARD; PRT; 87 AA.

AC P15811; P87353;

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Long neurotoxin CRI precursor (Kappa neurotoxin) (Kappa-3-

bungarotoxin) Many-banded krait).

OS Bungarus multicinctus (Many-banded krait).

OC Elapsoidea; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Bungarinae; Bungarus.

OX NCBI_TaxID=8616;

RN SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RA MEDLINE=9019201; PubMed=2315018;

RT "cDNA deduced amino-acid sequences of two novel kappa-neurotoxins

RT from Bungarus multicinctus.";

RN Nucleic Acids Res. 18:1050-1050(1990).

[2]

RP SEQUENCE FROM N.A.

RA Chang L.-S.; Lin J.- Hong E.;

RT "The exon-intron structure of kappa3-bungarotoxin precursor from

Taiwan banded krait."

RT Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

CC COMPARED TO ALPHA-NEUROTOXINS, KAPPA-3-BUNGAROTOXIN BIND MORE STRONGLY

CC TO NEURONAL RECEPTORS, AND LESS STRONGLY TO MUSCLE RECEPTORS.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the toxin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

CC or send an email to license@lsb-sib.ch).

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/

entities requires a license agreement (see <http://www.isb-sib.ch/announce> or send an email to license@isb-sib.ch).

CC EMBL; Z17665; CAA79029; 1; -.

CC DR EMBL; AAC05936; AAC97222; 1; -.

CC DR PIR; B84433; B84433.

CC DR HSSP; P202230; 1GFT.

CC DR InterPro; IPR002118; Gamma-thionin.

CC DR InterPro; IPR03614; Knot1.

CC DR Pfam; PF03030; Gamma-thionin; 1.

CC DR Prodom; PDO00594; G_Purothionin; 1.

CC DR SWISS; S900505; Knot1; 1.

CC DR PROSITE; PS00940; GAMMA_THIONIN; 1.

KW Plant defense; Signal; Multigene family.

SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 77 GAMMA-THIONIN HOMOLOG AT2G02120.

FT DISULFID 33 77 BY SIMILARITY.

FT DISULFID 44 64 BY SIMILARITY.

FT DISULFID 50 71 BY SIMILARITY.

FT DISULFID 54 73 BY SIMILARITY.

FT CONFLICT 19 19 V -> D (IN REF. 1).

FT CONFLICT 69 69 R -> G (IN REF. 1).

SEQUENCE 77 AA; 8578 MW; FBFBEBE5AF72A9A45 CRC64;

Query Match 8.8%; Score 47.5; DB 1; Length 77;

Best Local Similarity 28.6%; Pred. No. 1.6e-02;

Matches 18; Conservative 4; Mismatches 13; Gaps 2;

QY 18 GISSTTYVGRTCQSNSMIPHHWORTPEINYVAGLTENYCRNPD-----SGKQWCYNT 71

Db 22 GMGPVYVARTASQ-----QRFKCKVSDTNENYCHNEGFPGGDRCRGFRRCFCF 74

QY 72 DPC 74

Db 75 RNC 77

RESULT 15

	ATP8_PATCH	STANDARD	PRT;	55 AA.
AC	003168;			
DT	15-JUL-1998 (Rel. 36. Created)			
DT	15-JUL-1998 (Rel. 36. Last sequence update)			
DT	28-FEB-2003 (Rel. 41. Last annotation update)			
DE	ATP synthase protein 8 (EC 3.6.3.14) (Arpase subunit 8) (A6L).			
GN	MTATP8 OR ATP8.			
OS	Latimeria chalumnae (Latimeria) (Coelacanth).			
OG	Mitochondria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Coelacanthiformes; Coelacanthidae; Latimeria.			
OC	NCBI_TaxID=7897;			
RN	[1]			
RP	SEQUENCE FROM N A.			
RA	Zaridoya R., Meyer A.,			
RL	Submitted (DIC-1996) to the EMBL/GenBank/DDBJ databases.			
CC	-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF (0)) SUBUNIT OF THE MITOCHONDRIAL ATPASE COMPLEX.			
CC	-!- CATALYTIC ACTIVITY: ATP + H ⁽²⁺⁾ (In) = ADP + phosphate + H ⁽⁺⁾ (Out).			
CC	-!- SUBCELLULAR LOCATION: Membrane bound.			
CC	-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.			
CC	[2]			
CC	SEQUENCE FROM N A.			
CC	Zaridoya R., Meyer A.,			
CC	Submitted (DIC-1996) to the EMBL/GenBank/DDBJ databases.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC	EMBL; U82228; AAC60322; 1. -			
DR	PIR; E_88322; B58832.			
DR	InterPro; IPR01421; Arpase8 mit.			

DR Pfam; PF00895; ATP-synt_8; 1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 55 AA; 6559 MW; 7FE36319E8AF25B CRC44;
Query Match 8.7%; Score 47; DB 1; Length 55;
Best Local Similarity 31.7%; Pred. No. 1.3e+02;
Matches 13; Conservative 6; Mismatches 16; Indels 6; Gaps 3;
QY 31 SW---SSMPHWHQTENYNAAGTENCR-NPDSKQPW 67
|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 16 SWLITLMLPSKQL - HTEPNMPSTQNCKQEPPTWPW 54

Search completed: September 29, 2003, 08:20:19
Job time : 25 secs

Wed Oct 1 15:58:35 2003

us-10-088-548-4.sep29.rag

Page 9

Db 64 CHTNSQVRWEYCKTPSCS 82

Search completed: September 29, 2003, 08:19:47
Job time : 83 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:11:29 ; Search time 93 Seconds

(without alignments)
252.503 Million cell updates/sec

Title: US-10-088-548-4
Perfect score: 539
Sequence: 1 KSPVVODCYHGDGRSYRGTS.....DPCVRWEYCNLTQCSETESG 91

Scoring table: BLOSUM62
Gappp 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 118357

Minimum DB seq length: 0
Maximum DB seq length: 91

Post-processing: Maximum Match 0%
Maximum Match 0%
Listing first 45 summaries

Database :

```
SPTRIMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rhodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriop:*
17: sp_archaeap:*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

RESULT 1

Q9UMI2	PRELIMINARY;	PRT;	53 AA.
ID Q9UMI2;			
AC Q9UMI2;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE PLG protein (Fragment).			
GN PLG.			
OS Homo sapiens (Human).			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo			
OX NCBI_TAXID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=85023311; PubMed=6148961;			
RA Malinowski D.P., Sadler J.E., Davie E.W.;			
RT "Characterization of a complementary deoxyribonucleic acid coding for human and bovine Plasminogen.";			
RL Biochemistry 23:243-250(1984).;			
CC - SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.			
DR EMBL K02921; AAC0123..1; -			
DR HSSP; P00747; 2PK4.			
DR InterPro IPR00001; Kringle.			
DR PFAM; PF00051; kringle; 1			
DR PRINTS; PR00018; KRINGLE.			
DR PRODOM; PD000395; Kringle_1.			
DR SMART; SM00130; KR_1.			
DR PROSITE; PS00021; KRINGLE_1; FALSE_NEG.			
DR PROSITE; PS50070; KRINGLE_2; 1.			
KW Glycoprotein; Kringle.			
FT NON_TER 1 .. 1			
SQ SEQUENCE 53 AA; 5893 MW;			

Query Match 43.8%; Score 236; DB 4; Length 53;
Best Local Similarity 81.6%; Pred. No. 3 4e-19;
Matches 40; Consistency 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 SPVVQDCYHGDGRSYRGISSTVGTGTCQSWSMMPHWQTENPVNA 50

Result No.	Score	Query Match	Length	DB ID	Description
1	236	43.8	53	4 Q9UMI2	Q9UMI2 homo sapien
2	207.5	38.5	90	4 Q8V5I4	Q8V5I4 human resp
3	188	34.9	60	4 Q9JY3	Q9JY3 mus mucula
4	120.5	22.4	75	6 Q9UB3	Q9UB3 human resp
5	109	20.2	25	4 Q9TD88	Q9TD88 human resp
6	62	11.5	69	5 Q8V5I4	Q8V5I4 human resp
7	60.5	11.2	87	12 Q8V5I3	Q8V5I3 human resp
8	59.5	11.0	82	7 Q8V5I3	Q8V5I3 human resp
9	59.5	11.0	82	7 Q8V5I2	Q8V5I2 human resp
10	59	10.9	78	6 Q8V5I2	Q8V5I2 human resp
11	58.5	10.9	87	12 Q8V5I2	Q8V5I2 human resp
12	58.5	10.9	87	12 Q8V5I2	Q8V5I2 human resp
13	58	10.8	64	13 Q9UEF1	Q9UEF1 oncorhynchu
14	57.5	10.7	77	10 Q8V5I3	Q8V5I3 brassica ca
15	57.5	10.7	83	12 Q8V5I2	Q8V5I2 human resp
16	57.5	10.7	83	12 Q8V5I2	Q8V5I2 human resp

Db	5 : : : : : : : : : : : : : : : 5 TPyQDC7HGDCSYRRTSSSTTICKQCSWSSMTPHRQKTPENPVPA	DR SMART; SM00130; KR; 1. DR PROSITE; PS00021; KRINGLE_1; DR PROSITE; PS50070; KRINGLE_2; KW Glycoprotein; Kringle; Lipoprotein.
RESULT 2		
Q8NG20	PRELIMINARY;	PRT; 90 AA.
ID Q8NG20		
AC		
DT 01-OCT-2002 (TREMBrel. 22, Created)		
DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)		
DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)		
DE Plasminogen/activator Kringle.		
OS Homo sapiens (Human).		
OC Mammalia; Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Metazoa; Primates; Catarrhini; Hominidae; Homo.		
OX NCBI_TAXID=9606;		
RN [1].		
RP SEQUENCE FROM N.A.		
RA Dou D.		
RA "Production of kringle fragment."		
RL Submitted (JUN-2000) to the EMBL/CeNBank/DBJ databases.		
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.		
DR EMBL; AF282882; ARMS2248.1; .		
DR InterPro; IPR000001; Kringle.		
DR Pfam; PF00051; kringle; 1.		
DR PRINTS; PR000038; KRINGLE.		
DR ProDom; PD000395; Kringle; 1.		
DR SMART; SM00130; KR; 1.		
DR PROSITE; PS00021; KRINGLE_1; 1.		
DR PROSITE; PS50070; KRINGLE_2; 1.		
KW Glycoprotein; Kringle; Kringle.		
SQ SEQUENCE 90 AA; 9804 MW; A33887F9DF4C7B1 CRC64;		
Query Match 38.5%; Score 207.5; DB 4; Length 90;		
Best Local Similarity 47.6%; Pred. No. 9.2e-16;		
Matches 40; Conservative 14; Mismatches 25; Indels 5; Gaps 3;		
QY 7 DCYHGDSYRGISSTTTYGRTCWSWSPWPHQRTPEVNA---GL-TENYCRNPD 62		
7 : : : : : : : : : : : 7 DCYHGDSYRGISSTTTYGRTCWSWSPWPHQRTPEVNA---GL-TENYCRNPDG 65		
Db		
QY 63 GKQPCYTIDPCYRWEYCNLQCS 86		
63 : : : : : : : : 66 DAKPCYTINPRKLVDYCDVQCA 89		
Db		
RESULT 3		
Q9UKJ7	PRELIMINARY;	PRT; 60 AA.
ID Q9UKJ7		
AC Q9UKJ7;		
DT 01-MAY-2000 (TREMBrel. 13, Created)		
DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)		
DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)		
DE Apolipoprotein(a) (Fragment).		
GN apoA.		
OS Homo sapiens (Human).		
OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Buterilia; Primates; Catarrhini; Hominidae; Homo.		
OX NCBI_TAXID=9606;		
RN SEQUENCE FROM N.A.		
RX MEDLINE=2181705; PubMed=11285247;		
RA Ogorodikova M.; Kraut H.G.; Ehnholm C.; Uttermann G.;		
RT Single nucleotide polymorphisms in exons of the apo(a) Kringles IV		
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have		
RT different patterns in Africans and Caucasians.";		
RL Hum. Mol. Genet. 10:815-824 (2001).		
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.		
DR EMBL; AF158657; AF03576.1; .		
DR HSSP; P00747; IKN.		
DR InterPro; IPR000001; Kringle.		
DR Pfam; PF00051; kringle; 1.		
DR ProDom; PD000395; Kringle; 1.		
RESULT 5		
Q9UD88	PRELIMINARY;	PRT; 25 AA.
ID Q9UD88;		
AC Q9UD88;		
DT 01-MAY-2000 (TREMBrel. 13, Created)		
DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)		
DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)		
DE APO(A) KRINLE 4-37, APO(A) KRINLE type 5 (Fragment).		
OS Homo sapiens (Human).		
OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	Qy	72 DPCYRW 77
OC	Cercopitheciinae; Macaca.	Db	63 GTCEVN 68
OX	[1] NCBI_TaxID=9544;		
RN			
RC	SEQUENCE OF 3-30 FROM N.A.		
RF	TISSUE=Blood;		
RC	SEQUENCE OF 3-30 FROM N.A.		
RC	TISSUE=Blood;		
RC	MEDLINE:94179810; PubMed:81133043;		
RX	Sliedendregt B.L., Otting N., van Besouw N., Jonker M., Bontrop R.E.;		
RT	"Expansion and contraction of rhesus macaque DRB regions by duplication and deletion."		
RT	J. Immunol. 152:2298-2307(1994).		
RN	[2] 12098-2307(1994).		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood;		
RA	de Groot N.N.;		
RL	Submitted (Oct-1997) to the EMBL/GenBank/DBJU databases.		
DR	AF031268; AB874401; -.		
DR	HSSP; P13758; IDLH.		
DR	InterPro; IPR00353; MHC_II_beta.		
DR	Pfam; PF00965; MHC_II_beta; 1.		
DR	ProDom; PD000328; MHC_II_beta; 1.		
KW	Glycoprotein; MHC II; Transmembrane.		
FT	NON_TER 82 82		
FT	SEQUENCE 82 AA; 9960 MW; 71FA3A6520A60119 CRC64;		
Query Match	11.0%; Score 59.5; DB 7; Length 82;		
Best Local Similarity	30.8%; Pred. No. 29;		
Matches	16; Conservative 8; Mismatches 17; Indels 11; Gaps 3;		
Qy	9 YHGDDGRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPNAGL-TEINYCRN 59		
Db	33 FDSDGEYRAVE -LGRPPAESNSQRDYLEKRAE-----VDNCRH 74		
RESULT 10			
Q8SQ084	PRELIMINARY;	Qy	1 KSPVQDCYHGDRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPN 49
ID	Q8SQ084	ID	1 KSPVQDCYHGDRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPN 49
AC	Q8SQ084;	AC	1 KSPVQDCYHGDRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPN 49
DT	01-JUN-2002 (TREMBLrel. 21, Created)	Db	21 KKPPPKTERGTSTOSVLDTTSKETIQQS---IJSITPENTPN 64
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	MHC_G (Fragment).		
GN	MHC_G.		
OS	Gorilla gorilla (gorilla).		
RA	Euitazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.		
OX	NCBI_TaxID=9593;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	MEDLINE:973668; PubMed:9218527;		
RA	Araiza-Villena A., Martinez-Laso J., Alvarez M., Castro M.J.,		
RA	Varela P., Gomez-Casado E., Suarez B., Recio M.J., Vargas-Alarcon G.,		
RA	Morales P.,		
RT	"Primate Mhc-8 and -G alleles."		
RT	Immunogenetics 46:251-266(1997).		
DR	EMBL; [141256]; ARI77572.1;		
DR	InterPro; IPR001039; MHC_I.		
DR	Pfam; PF00129; MHC_I; 1.		
DR	ProDom; PD000050; MHC_I; 1.		
FT	NON_TER 1 1		
FT	SEQUENCE 78 AA; 8891 MW; EC12DFF3A58FC7B3 CRC64;		
Query Match	10.9%; Score 59; DB 6; Length 78;		
Best Local Similarity	22.7%; Pred. No. 31;		
Matches	15; Conservative 10; Mismatches 37; Indels 4; Gaps 1;		
Qy	12 DGTSRQISSTTVGR-TGQSWSSMTPHWHORTPEYNPNAGL-TEINYCRN 71		
Db	7 DSRLLRGQEYAYDGKDYLALNEDLSWTAADTA---AQISKRKEAPNASEQRAYLE 62		
RESULT 11			
Q8BBBA5	PRELIMINARY;	Qy	1 KSPVQDCYHGDRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPN 49
ID	Q8BBBA5	ID	1 KSPVQDCYHGDRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPN 49
AC	Q8BBBA5;	AC	1 KSPVQDCYHGDRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPN 49
DT	01-MAR-2003 (TREMBLrel. 23, Created)	Db	21 KKPPPKTERGTSTOSVLDTTSKETIQQS---IJSITPENTPN 64
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Glycoprotein (Fragment).		
GN	GN		
OS	Human respiratory syncytial virus.		
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;		
OC	Paramyxoviridae; Pneumovirinae; Pneumovirus.		
OX	NCBI_TaxID=11250;		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=9K6-99;		
RA	MEDLINE=22213634; PubMed:12226836;		
RA	Venter M., Collinson M., Schoub B.D.;		
RA	"Molecular epidemiological analysis of community circulating respiratory syncytial virus in rural South Africa: Comparison of viruses and genotypes responsible for different disease manifestations."		
RA	J. Med. Virol. 68:452-451(2002).		
DR	EMBL; AF548806; AAN62463.1; -.		
FT	NON_TER 1 1		
FT	SEQUENCE 87 AA; 9431 MW; F72B9DC59C975EE0 CRC64;		
Query Match	10.9%; Score 58.5; DB 12; Length 87;		
Best Local Similarity	32.7%; Pred. No. 40;		
Matches	16; Conservative 3; Mismatches 25; Indels 5; Gaps 1;		
Qy	1 KSPVQDCYHGDRSYRGISSITVGR-TGQSWSSMTPHWHORTPEYNPN 49		

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:22:53 ; Search time 82 Seconds

(without alignments)
172.216 Million cell updates/sec

Title: US-10-088-548-6

Perfect score: 523
Sequence: 1 VRQCYHNGQSYRGTFSTVV.....SURVEYNLTRCSDTETGVV 89

Scoring table: BJOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs 158726573 residues

Total number of hits satisfying chosen parameters:

693114

Minimum DB seq length: 0

Maximum DB seq length: 89

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03:^{*}

- 1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2004.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed,

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	523	100.0	89	22 AAY72946	Human apolipoprotein
2	430	82.2	84	21 AAY77720	Human plasminogen
3	427	81.6	82	10 AAP93231	Plasminogen kringl
4	421	80.5	83	21 AAB08414	Amino acid sequenc
5	417	79.7	78	17 AAV07560	Human kringle 4.
6	369	70.6	78	17 AAV07559	Murine kringle 4.
7	349.5	66.8	86	23 AAB02801	Human ORF8 protein
8	313	59.8	78	17 AAV07554	Murine kringle 3.
9	299	57.2	78	17 AAV07557	Porcine kringle 3.

Homo sapiens.

PN WO200119868-A1.

XX PD 22-MAR-2001.

XX PP 15-SEP-1999;

XX PR 15-SEP-1999;

XX PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

XX PI Chang J, Kim JS, Park EJ, Yum J, Chung S;

XX DR WPI; 2001-24478/25.

DR N-PSDB; AAD03257.

ALIGNMENTS

RESULT 1	ARY72946	standard; Protein; 89 AA.
XX	XX	ID AAY72946
XX	XX	DT 13-JUN-2001 (first entry)
XX	XX	DE Human apolipoprotein(a) kringle domain IV37, LK7 protein.
XX	XX	KW Human angiogenesis inhibitor; LK7; apolipoprotein(a) kringle domain; angiogenesis inhibitor; cancer; rheumatoid arthritis; therapy; cytotoxic; antirheumatic; antiarthritic; antipsoriatic; psoriasis; ocular angiogenic disease; endothelial cell proliferation; tumour; cell migration.
XX	XX	OS Homo sapiens.
XX	XX	PN WO200119868-A1.
XX	XX	PD 22-MAR-2001.
XX	XX	PP 15-SEP-1999;
XX	XX	PR 15-SEP-1999;
XX	XX	PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
XX	XX	PI Chang J, Kim JS, Park EJ, Yum J, Chung S;
XX	XX	DR WPI; 2001-24478/25.
XX	XX	DR N-PSDB; AAD03257.

XX Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -
XX Claim 2; Page 45-46; 50pp; English.
PS The present sequence is human LK7 protein which contains the amino
XX acid sequence of human apolipoprotein(a) kringle domain IV37
CC (LK7). The human apolipoprotein(a) kringle domains IV36 (LK6
CC protein), IV7 (LK7 protein) and V38 (LK8 protein) together form the
CC angiogenesis inhibitor, LK68 protein. LK68 protein, LK6, LK7 and LK8 are
CC inhibitors of endothelial cell proliferation, cell migration and
CC normal development of capillaries in the chick embryo chorioallantoic
CC membrane (CAM). LK68 protein, its single kringle or their functional
CC equivalents, are useful for treating angiogenesis-mediated diseases,
CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC disease in animals or humans. LK68 is useful as an anticancer agent and
CC also for inhibiting primary tumour growth.
XX Sequence 89 AA;

Query Match 100.0%; Score 523; DB 22; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.2e-46;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
Do 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
Do 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89

RESULT 2
ID AAY77720 standard; peptide: 84 AA.

XX AAY77720;
XX AC AAY77720;
XX DT 12-MAY-2000 (first entry)

DE Human plasminogen kringle 4 sequence.

XX Kringle 4; Plasminogen; anti-angiogenic; angiogenesis; angiostatin;
KW cytostatic; antiarthritic; antirheumatic; anidiabetic; ophthalmological;
KW immunosuppressant; vasoactive; vulnerable; antiarteriosclerotic; human;
KW dermatologic; cancer; tumour; birth control; vascularization.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Region 59..75
FT /note= "specifically claimed fragment (AAY77723)"
XX XX WO200003726-A1.
XX PD 27-JAN-2000.
XX PF 07-JUL-1999; 99WO-US15271.
XX PR 14-JUL-1998; 98US-009231.
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX PI Ji R, Trail PA;
XX DR WPI; 2000-171200/15.
XX PT Novel lysine binding fragments angiostatin used as antiangiogenic
PT agents in the treatment of cancer, diabetic retinopathy, rheumatoid
PT arthritis, psoriasis, atherosclerotic plaque formation, and other
antiangiogenesis diseases -

PT Disclosure; Fig 3; 30pp; English.
XX PS
XX CC The invention provides fragments of kringle 1, 2 or 4 of human
CC plasminogen that contain a lysine binding site and have anti-angiogenic
CC activity. The peptides of the invention function as antiangiogenic
CC agents, for the treatment process and diseases involving angiogenesis.
CC Such diseases include cancers such as solid tumours, blood born tumours
CC such as leukemias, tumours metastasis, benign tumours such as
CC hemangiomas, acoustic acromas, neurofibromas, trachomas and pyogenic
CC granulomas, rheumatoid arthritis, ocular angiogenic diseases such as
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC ruberosis, Osler-Weber syndrome, myocardial angiogenesis, plaque
CC neovascularization, telangiectasias, hemophilic joints, angiofibroma,
CC and wound granulation. The fragments are also useful in treatment of
CC disease of excessive or abnormal stimulation of endothelial cells. These
CC diseases include intestinal adhesions, atherosclerosis, scleroderma, and
CC hypertrophic scars. The fragments can be used as birth control agents by
CC preventing vasculization required for embryo transplantation. The
CC present sequence represents the kringle 4 sequence of human plasminogen
CC (angiostatin).

XX SQ Sequence 89 AA;
XX Query Match 100.0%; Score 523; DB 22; Length 84;
XX Best Local Similarity 83.3%; Pred. No. 1.5e-36;
XX Matches 70; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

XX Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
XX Db 1 YQDCYHGDGSYRTSSTTTKKCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

XX Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
XX Db 61 GEWCFTDPSIRWEYCNLTCSDTEGVV 89

XX RESULT 3
ID AAY93231 standard; peptide: 82 AA.
XX ID AAY93231;
XX AC AAY93231;

XX Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
XX Db 1 YQDCYHGDGSYRTSSTTTKKCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

XX Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
XX Db 61 GEWCFTDPSIRWEYCNLTCSDTEGVV 89

XX RESULT 4
ID AAY93231 standard; peptide: 82 AA.
XX ID AAY93231;
XX AC AAY93231;

XX Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
XX Db 1 YQDCYHGDGSYRTSSTTTKKCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

XX Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
XX Db 61 GEWCFTDPSIRWEYCNLTCSDTEGVV 89

XX RESULT 5
ID AAY93231 standard; peptide: 82 AA.
XX ID AAY93231;
XX AC AAY93231;

XX Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
XX Db 1 YQDCYHGDGSYRTSSTTTKKCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

XX Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
XX Db 61 GEWCFTDPSIRWEYCNLTCSDTEGVV 89

XX RESULT 6
ID AAY93231 standard; peptide: 82 AA.
XX ID AAY93231;
XX AC AAY93231;

XX Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
XX Db 1 YQDCYHGDGSYRTSSTTTKKCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

XX Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
XX Db 61 GEWCFTDPSIRWEYCNLTCSDTEGVV 89

XX RESULT 7
ID AAY93231 standard; peptide: 82 AA.
XX ID AAY93231;
XX AC AAY93231;

XX Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
XX Db 1 YQDCYHGDGSYRTSSTTTKKCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

XX Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
XX Db 61 GEWCFTDPSIRWEYCNLTCSDTEGVV 89

XX RESULT 8
ID AAY93231 standard; peptide: 82 AA.
XX ID AAY93231;
XX AC AAY93231;

XX Qy 1 VRQCYHNGQSTRGRTTGTGRCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60
XX Db 1 YQDCYHGDGSYRTSSTTTKKCQSSWMMTPHRQRTENTPNDGTTMNYCRNPDADT 60

XX Qy 61 GPWCFTDPSIRWEYCNLTCSDTEGVV 89
XX Db 61 GEWCFTDPSIRWEYCNLTCSDTEGVV 89

XX Disclosure; fig 3b; 80pp; English.

XX The sequence is encoded by a synthetic oligonucleotide and is the kringle 4 domain of plasminogen. It is used to construct a modified plasminogen activator (mpA) of greater fibrin selectivity than normal PA. The mPA is used in the treatment of pulmonary embolism, thrombosis, myocardial infarct and strokes.

(Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 82 AA;

Query Match 81.6%; Score 427; DB 10; Length 82;

Best Local Similarity 85.2%; Pid: No. 3.le-36; Indels 0; Gaps 0;

Matches 69; Conservative 7; Mismatches 0;

QY 1 VRQCYHNGOSYRTGTSVTPVIGRTCSWSSMTPHRQKTPENYPNDGLTMNYCRNPDAK 60

2 VQDCYHNGOSYRTGTSVTPVIGRTCSWSSMTPHRQKTPENYPNDGLTMNYCRNPDAK 61

Db 61 GPWCFTTDPSIRVEYCNIKTRC 81

62 GPWCFTTDPSIRVEYCNIKRC 82

RESULT 4

AA08414 ID AAB08414 standard; Protein: 83 AA.

AC AAB08414;

XX DT 20-DEC-2000 (first entry)

XX DE Amino acid sequence of kringle 4 of human plasminogen.

XX KW Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA; tissue plasminogen activator; tumour; therosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distress syndrome; Castlemann's disease; Psoriasis; hepatitis; aneurysm; renal disease; haemangiomia.

XX OS Homo sapiens.

XX PN WO200049871-A1.

PD 31-AUG-2000.

XX PF 24-FEB-2000; 2000WO-US04798.

XX PR 24-FEB-1999; 99US-0121341.

PT 25-FEB-1999; 99US-0121633.

XX 18-NOV-1999; 99US-0166176.

PA (FORD-) FORD HEALTH SYSTEM HENRY.

XX PI Dou D, Chopp M, Wang L, Mikkelsen T;

XX DR WPI; 2000-572016/53.

XX PS Disclosure; Fig 6; 163pp; English.

CC The specification describes a human polypeptide which is a potent angiogenesis inhibitor, and is designated KED. KED polypeptide, kringle proteins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome,

CC Castleman's disease, psoriasis, hepatitis, aneurysm, renal disease and haemangioma. The present sequence represents kringle 4 of human plasminogen, which is used in the course of the invention.

XX Sequence 83 AA;

Query Match 80.5%; Score 421; DB 21; Length 83;

Best Local Similarity 84.1%; Pid: No. 1.3e-35;

Matches 69; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 VRQCYHNGOSYRTGTSVTPVIGRTCSWSSMTPHRQKTPENYPNDGLTMNYCRNPDAK 60

1 VQCYHNGOSYRTGTSVTPVIGRTCSWSSMTPHRQKTPENYPNDGLTMNYCRNPDAK 60

Db 61 GPWCFTTDPSIRVEYCNIKRC 82

61 GPWCFTTDPSIRVEYCNIKRC 82

RESULT 5

AAW07560 ID AAW07560 standard; protein: 78 AA.

AC AAW07560;

XX DT 22-JUN-1997 (first entry)

XX DE Human kringle 4.

XX KW angiotatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.

XX OS Homo sapiens.

XX PN WO9655774-A2.

XX PD 14-NOV-1996.

XX PR 26-APR-1996; 96WO-US05856.

XX PR 08-MAR-1996; 96US-061278.

PR 26-APR-1995; 95US-0429743.

PR 22-FEB-1996; 95US-0605598.

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;

XX DR WPI; 1996-518662/51.

XX PR Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis mediated diseases, e.g. cancer, arthritis or diabetic retinopathy.

XX XX Claim 4; Page 11; 203pp; English.

CC The invention relates to new methods and compositions for inhibiting endothelial cell proliferation using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine Plasminogen. The active component is a kringle 1, kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4BKUS protein. The aggregate angiostatin has a Mol. wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine Plasminogen. The active component can be used for treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

CC The present sequence, human kringle 4, is a specific angiostatin fragment which can be used in the invention.

XX Sequence 78 AA;

Query Match 79.7%; Score 417; DB 17; Length 78;
 Best Local Similarity 85.9%; Pred. No. 3e-35;
 Matches 67; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 CYHGNQSYRGFSTVTGRTCSWSMTPHRQHTPENYPNDGLTMNCRNPDAUTGPW 63
 Db 1 CYHGDQSYRGISSTTGRKQCSWSMTPHRQTPENYNAGLTMNCRNPDAKGPKW 60

QY 64 CFTTDPSRWEYCNLRC 81
 Db 1 CFTTDPSRWEYCNLKC 78

RESULT 6
 AAW07559 standard; protein; 78 AA.
 XX
 ID AAW07559
 AC AAW07559;
 XX
 DT 22-JUN-1997 (first entry)
 XX
 DE Murine kringle 4.
 XX
 KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 KW macular degeneration; diabetic retinopathy.
 XX
 OS Mus musculus.
 XX
 PN WO9655774-A2.
 XX
 PD 14-NOV-1996.
 XX
 PF 26-APR-1996; 9WO-US050556.
 XX
 PR 08-MAR-1996; 96US-0612788.
 PR 26-APR-1995; 95US-0429443.
 PR 22-FEB-1996; 96US-060598.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CBN.
 XX
 PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;
 XX
 DR WPI; 1996-518662/51.
 XX
 PT Use of angiostatin fragments or aggregates - for inhibiting
 PT endothelial cell proliferation and treating angiogenesis-mediated
 PT diseases, e.g. cancer, arthritis or diabetic retinopathy
 PS Claim 4; Page 115; 203pp; English.
 XX
 CC The invention relates to new methods and compositions for
 CC inhibiting endothelial cell proliferation, using as active component
 CC an angiostatin fragment, a combination of angiostatin fragments, or
 CC aggregate angiostatin. The fragment is preferably derived from murine,
 CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
 CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
 CC 1-4 or kringle 1-4BKTS protein. The aggregate angiostatin has a Mr. Wt.
 CC of 45-65 kD and is derived from a plasminogen fragment beginning at number
 CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
 CC bovine plasminogen. The active component can be used for treating
 CC angiogenesis-mediated diseases such as cancer, arthritis, macular
 CC degeneration and diabetic retinopathy. It can also be used to develop
 CC antibodies for use in diagnosis, detection and therapy.
 CC The present sequence, murine kringle 4, is a specific angiostatin
 CC fragment which can be used in the invention, and represents amino
 CC acids 377-454 of murine plasminogen.
 XX
 Sequence 78 AA;

Query Match 70.6%; Score 368; DB 17; Length 78;
 Best Local Similarity 73.1%; Pred. No. 2.4e-10;
 Matches 57; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 4 CYHGNQSYRGFSTVTGRTCSWSMTPHRQHTPENYPNDGLTMNCRNPDAUTGPW 63
 Db 1 CYQSDQSYRGFSTVTGRCQSWAMPFHRSKTPENFDAGLEMNTCRNPDGKGPKW 60

QY 64 CFTTDPSRWEYCNLRC 81
 Db 1 CYTTDPSPRWEYCNLKC 78

RESULT 7
 ABP02801 standard; protein; 86 AA.
 XX
 ID ABP02801
 AC ABP02801;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Human ORFX protein sequence SEQ ID NO:5584.
 XX
 KW Human; open reading frame; ORFX; gene; therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.

XX
 OS Homo sapiens.

XX
 PN WO200192523-A2.

XX
 PD 06-DEC-2001.

XX
 PR 29-MAY-2001; 2001WO-US10836.

XX
 PR 30-MAY-2000; 2000US-206132P.

PR 29-AUG-2000; 2000US-238716P.

XX
 PA (CURA-) CURAGEN CORP.

XX
 PI Shimkets RA, Leach MD;

XX
 DR WPI; 2002-106308/14.

DR N-PSDB; ABN1853.

XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders

XX
 PS Disclosure; SEQ ID 5584; 1037pp; English.

XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN7252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, circrosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infections
 CC diseases, autoimmune disorders such as multiple sclerosis, rhusumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,

CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_bot_sequences.

SQ Sequence 86 AA;
Query Match 66.8%; Score 349.5; DB 23; Length 86;
Best Local Similarity 73.4%; Pred. No. 2.7e-28;
Matches 58; Conservative 8; Mismatches 12; Indels 1; Gaps 1;
XX QY 1 VRQCHGNGOSYRTTESTVGRTCQSWSMTPHRHQPTPENPNPDGLTNYCRNPAD-
Db 7 YOECYHGNGOSYRTTESTVGRKCCSQWSNTPSHSTPANFDAGLENNYCRNPADQ 66
QY 60 TGPWCFTTDPSIRWEYCNL 78
Db 67 RSPWCFTTDPSVREYCNL 85

RESULT 8
AAW07554 standard; protein: 78 AA.
XX AC AAW07554;
XX DT 21-JUN-1997 (first entry)
DE Porcine kringle 3.
XX DE 21-JUN-1997 (first entry)
DE Murine kringle 3.
XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
KW macular degeneration; diabetic retinopathy.
XX OS Sus scrofa.
XX PN WO9635774-A2.
OS Mus musculus.
XX PN WO9635774-A2.
XX PD 14-NOV-1996.
XX PD 14-NOV-1996.
XX PP 26-APR-1996; 96WO-US05856.
XX PR 08-MAR-1996; 96US-0612788.
XX PR 08-MAR-1996; 96US-0612788.
PR 26-APR-1995; 95US-0429743.
PR 22-FEB-1996; 96US-060598.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Cao Y, Folkman MJ, Lin J, O'reilly MS, Sim KL;
XX PI Cao Y, Folkman MJ, Lin J, O'reilly MS, Sim KL;
XX DR 1996-518662/51.

XX Use of angiostatin fragments or aggregates - for inhibiting angiogenesis-mediated
PT endothelial cell proliferation and treating angiogenesis-mediated
PT diseases, e.g. cancer, arthritis or diabetic retinopathy
XX
PS Claim 4; Page 111; 203pp; English.
XX
The invention relates to new methods and compositions for
CC inhibiting endothelial cell proliferation, using as active component
CC an angiostatin fragment, a combination of angiostatin fragments, or
CC aggregate angiostatin. The fragment is preferably derived from murine,
CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
CC 1-4 or kringle 1-4BKLIS protein. The aggregate angiostatin has a Mol. Wt.
CC of 45-65 kD and is derived from a plasminogen fragment beginning at
CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
CC bovine plasminogen. The active component can be used for treating
CC angiogenesis-mediated diseases such as cancer, arthritis, macular
CC degeneration and diabetic retinopathy. It can also be used to develop
CC antibodies for use in diagnosis, detection and therapy.
CC The present sequence, porcine kringle 3, is a specific angiostatin
CC fragment which can be used in the invention, and represents amino
CC acids 178-255 of porcine angiostatin.
XX SQ Sequence 78 AA;

CC acids 275-352 of murine plasminogen or amino acids 178-255 of murine
CC angiostatin.
XX SQ Sequence 78 AA;
Query Match 59.8%; Score 313; DB 17; Length 78;
Best Local Similarity 61.5%; Pred. No. 1.3e-24;
Matches 48; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
XX QY 4 CYHNGQSYRTGSTVGRTCQSWSMTPHRHQPTPENPNPDGLTNYCRNPAD-
Db 1 CLKGKGNERYGRIVSIVTSGKTCQRNSQTPHRHNRTPENPICKNLENVCRNPDGTFAPW 60
QY 64 CFTTDPSPTRWEYCNLAC 81
Db 61 CYTIDSQLRWEYCEIPS 78
RESULT 9
AAW07557
ID AAW07557 standard; protein: 78 AA.
XX AC AAW07557;
XX DT 21-JUN-1997 (first entry)
XX DE Porcine kringle 3.
XX DE 21-JUN-1997 (first entry)
DE Porcine kringle 3.
XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
KW macular degeneration; diabetic retinopathy.
XX OS Sus scrofa.
XX PN WO9635774-A2.
OS Mus musculus.
XX PN WO9635774-A2.
XX PD 14-NOV-1996.
XX PD 26-APR-1996;
XX PP 26-APR-1996; 96WO-US05856.
XX PR 08-MAR-1996; 96US-0612788.
XX PR 26-APR-1995; 95US-0429743.
XX PR 22-FEB-1996; 96US-060598.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Cao Y, Folkman MJ, Lin J, O'reilly MS, Sim KL;
XX WPI; 1996-518662/51.
XX PT Use of angiostatin fragments or aggregates - for inhibiting angiogenesis-mediated
PT endothelial cell proliferation and treating angiogenesis-mediated
PT diseases, e.g. cancer, arthritis or diabetic retinopathy
XX PS Claim 4; Page 113-114; 203pp; English.
XX CC The invention relates to new methods and compositions for
CC inhibiting endothelial cell proliferation, using as active component
CC an angiostatin fragment, a combination of angiostatin fragments, or
CC aggregate angiostatin. The fragment is preferably derived from murine,
CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
CC kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
CC 1-4 or kringle 1-4BKLIS protein. The aggregate angiostatin has a Mol. Wt.
CC of 45-65 kD and is derived from a plasminogen fragment beginning at
CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
CC bovine plasminogen. The active component can be used for treating
CC angiogenesis-mediated diseases such as cancer, arthritis, macular
CC degeneration and diabetic retinopathy. It can also be used to develop
CC antibodies for use in diagnosis, detection and therapy.
CC The present sequence, porcine kringle 3, is a specific angiostatin
CC fragment which can be used in the invention, and represents amino
CC acids 178-255 of porcine angiostatin.
XX SQ Sequence 78 AA;

Query Match 57.2%; Score 299; DB 17; Length 78;
 Best Local Similarity 56.4%; Pred No. 3 5e-13;
 Matches 44; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.

XX

SQ Sequence 83 AA;

Query Match 54.7%; Score 286; DB 21; Length 83;
 Best Local Similarity 55.7%; Pred. No. 7.9e-22;
 Matches 44; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 3 QCYHGNGQSQRGFTSTTGTGTCQSNSSMPHRQHPTENPNDGLITMYCRNPDAADTP 62
 | :| :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 DE 3 QCLKGEGENTGRNVTAVYTSQHTCQHNSAQTPHTNRTPENFPCKNLDEYCRNEGDGKAP 62

Db

QY 63 WQETTDPSPISRWEYCNLTIC 81
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 DB 63 WCHTINNSQVRWEYCKIPSC 81

RESULT 1.0

AAB01908 ID AAB01908 standard; Protein; 83 AA.

XX

AC AAB01908;

XX DT 18-SEP-2000 (first entry)

XX DE Human plasminogen kringle 3 (Thr253-Ser335).

XX KW Plasminogen; human; kringle domain; endothelial cell proliferation; antiproliferative; antiangiogenesis; antiarteriosclerotic; cytostatic; antiinflammatory; anticancer; antidiabetic; antidiabetic; antiangiogenic; antidiabetic; antiangiogenic; anticancer; tumour; autoimmune disease.

XX KW Homo sapiens.

OS US6057122-A.

XX PN PA (CHIL) CHILDRENS MEDICAL CNT.

XX PD 02-MAY-2000.

XX PP 05-MAY-1997; 97US-0851350.

XX PR 03-MAY-1996; 96US-0643219.

XX PR 03-APR-1997; 97US-0832087.

XX PA (ABB0) ABBOTT LAB.

PI Davidson DJ;

XX DR WPI; 2000-349573/30.

XX PT Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian Plasminogen and elastase followed by incubation and isolation.

XX PS Example 17; Page -; 48pp; English.

XX CC The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian Plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haemopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases, blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.

CC Note: This sequence is not shown in the specification, but is derived

XX CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.

XX

SQ Sequence 83 AA;

RESULT 1.1

AAW07555 ID AAW07555 standard; Protein; 78 AA.

XX AC AAW07555;

XX DT 21-JUN-1997 (first entry)

XX DE Human kringle 3.

XX KW angiotatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.

XX OS Homo sapiens.

XX PN WO9635774-A2.

XX PD 14-NOV-1996.

XX PF 26-APR-1996; 96WO-US058556.

XX PR 08-MAR-1996; 96US-0612783.

XX PR 26-APR-1995; 95US-0429743.

XX PR 22-FEB-1996; 96US-0605598.

XX PA (CHIL-) CHILDRENS MEDICAL CNT.

XX PI Cao Y, Folkman MJ, Lin J, Oreilly MS, Sim KJ;

XX DR WPI; 1996-518662/51.

XX PT Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy.

XX PS Claim 4; Page 112; 203pp; English.

XX CC The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or an angiostatin fragment. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 2-3, kringle 1-2, Kringle 1-4 or kringle 1-4BKLs protein. The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

CC The present sequence, human kringle 3, is a specific angiostatin fragment which can be used in the invention, and represents amino acids 178-255 of human angiostatin.

XX Sequence 78 AA;

XX SQ

Query Match Similarity 54.5%; Score 285; DB 17; Length 78;
 Best Local Similarity 55.1%; Pred. No. 9, 3e-22; Mismatches 25; Indels 0; Gaps 0;
 Matches 43; Conservative 10;

QY 4 CYHNGQSRYGTFSTIVTGRICQWSMTPHRQTPENYPNDGLIMNYCRNPDAUTGPW 63
 DB 1 CLKGTGENRGDYAVTSGHTCHGSQAQPTPHNRTPEFCKNLDENYCRNPGEKAPW 60

QY 64 CTTTDSIRKEYCNCITRC 81
 DB 61 CTTTNSQRWEYCKIPSC 78

RESULT 1.2

AAW07556 ID AAW07556 standard; protein; 78 AA.
 XX AC AAW07556;
 XX DT 21-JUN-1997 (first entry)
 DE Rhesus kringle 3.
 XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 KW macular degeneration; diabetic retinopathy.
 DE Bos taurus.
 XX OS Bos taurus.
 XX PN WO9635774-A2.
 XX PD 14-NOV-1996.
 XX PR 26-APR-1996; 96WO-US05856.
 XX PR 14-NOV-1996.
 XX PR 26-APR-1996; 96US-0612788.
 XX PR 08-MAR-1996; 96US-0429743.
 XX PR 26-APR-1995; 95US-0429743.
 XX PR 22-FEB-1996; 96US-0605598.
 XX PR (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;
 XX DR WPI; 1996-518662/51.

Use of angiostatin fragments or aggregates - for inhibiting
 endothelial cell proliferation and treating angiogenesis-mediated
 diseases, e.g. cancer, arthritis or diabetic retinopathy

Claim 4; Page 114; 203pp; English.

PT Use of angiostatin fragments or aggregates - for inhibiting
 PT endothelial cell proliferation and treating angiogenesis-mediated
 PT diseases, e.g. cancer, arthritis or diabetic retinopathy

PS Claim 4; Pages 112-113; 203pp; English.

The invention relates to new methods and compositions for
 inhibiting endothelial cell proliferation, using as active component
 an angiostatin fragment, a combination of angiostatin fragments, or
 aggregate angiostatin. The fragment is preferably derived from murine,
 human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
 kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle
 1-4 or kringle 1-4BKLS protein. The aggregate angiostatin has a Mol. Wt.
 of 45-65 kD and is derived from a plasminogen fragment beginning at
 approximately amino acid number 98 of murine, human, Rhesus, porcine or
 bovine plasminogen. The active component can be used for treating
 angiogenesis-mediated diseases such as cancer, arthritis, macular
 degeneration and diabetic retinopathy. It can also be used to develop
 antibodies for use in diagnosis, detection and therapy. The present sequence,
 bovine kringle 3, is a specific angiostatin fragment which can be used in the invention, and represents amino acids 178-255 of bovine angiostatin.

SQ Sequence 78 AA;

Query Match Similarity 53.7%; Score 281; DB 17; Length 78;
 Best Local Similarity 53.8%; Pred. No. 2.4e-21; Mismatches 25; Indels 0; Gaps 0;
 Matches 42; Conservative 11;

QY 4 CYHNGQSRYGTFSTIVTGRICQWSMTPHRQTPENYPNDGLIMNYCRNPDAUTGPW 63
 DB 1 CLKGTGENRGDYAVTSGHTCHGSQAQPTPHNRTPEFCKNLDENYCRNPGEKAPW 60

QY 64 CFTIDPSIRWEYCNLTRC 81
|:|||:|||:|||:|||:
Db 61 CYTINSEVRWEYCTIPSC 78

RESULT 14
ID AAW0753 standard; protein; 78 AA.
XX
AC AAW0753;
XX DT 21-JUN-1997 (first entry)
DE Bovine kringle 2.
XX angiotatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
KW macular degeneration; diabetic retinopathy.
XX OS Bos taurus.
XX PN WO9635774-A2.
XX PD 14-NOV-1996.
XX PF 26-APR-1996; 96WO-US05856.
XX PR 08-MAR-1986; 96US-061288.
PR 26-APR-1995; 95US-042943.
PR 22-FEB-1986; 96US-0605598.
XX PA (CHIL) CHILDRENS MEDICAL CENT.
XX PI Cao Y, Folkman MJ, Lin J, O'Reilly MS, Sim KL;
DR WPI; 1996-518862/51.
XX PT Use of angiostatin fragments or aggregates - for inhibiting
endothelial cell proliferation and treating angiogenesis-mediated
PT diseases, e.g. cancer, arthritis or diabetic retinopathy.
XX PS Claim 4: Page 110; 203pp; English.
XX The invention relates to new methods and compositions for
CC inhibiting endothelial cell proliferation, using as active component
CC an angiostatin fragment, a combination of angiostatin fragments, or
CC aggregate angiostatin. The fragment is preferably derived from murine,
CC human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
CC 2, kringle 3, kringle 2-3, kringle 1-2, kringle 1-4 or kringle 1-BKLS protein.
CC The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at
CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
CC bovine plasminogen. The active component can be used for treating
CC angiogenesis-mediated diseases such as cancer, arthritis, macular
CC degeneration and diabetic retinopathy. It can also be used to develop
CC antibodies for use in diagnosis, detection and therapy.
CC The present sequence, bovine kringle 2, is a specific angiostatin
CC fragment which can be used in the invention, and represents amino
CC acids 88-165 of bovine angiostatin.
XX Sequence 78 AA;

Query Match 53.0%; Score 277; DB 17; Length 78;
Best Local Similarity 52.6%; Pred. NO. 6.1e21;
Matches 41; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 4 CYHNGQSRYGTFSTTYGRCQSHSSMTPHRQRTPENYPNDGTMNCRNPDAITGPW 63
|:|||:|||:|||:|||:|||:|||:|||:|||:
Db 1 CMHCSEGTEGKTAKTSGRCQAWDSSOPHAGLYTKEFKNKLMYCRNPGEPRPW 60

QY 64 CFTIDPSIRWEYCNLTRC 81
|:|||:|||:|||:|||:
Db 61 CFTIDPQKRMFCDIPRC 78

QY 3 QCYHGNGQSRYGTFSTTYGRCQSHSSMTPHRQRTPENYPNDGTMNCRNPDAITGP 62
|:|||:|||:|||:|||:|||:|||:|||:|||:
Db 3 QCJKKGEGENTRGNNAVTSGSICQHNSAQPHTANRTEFNFCQKNULDENYCQNPDDGKRAP 62

QY 63 WCFTTDPDSIRWEYCNLTRCS 82
|:|||:|||:
Db 63 WCHTTNSQVRWEICKTPSCS 82

Search completed: September 29, 2003, 08:33:33
Job time : 83 secos

COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE:
 TELECOMMUNICATION INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REFERENCE/DOCKET NUMBER: 05940-0251
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..78
 OTHER INFORMATION: /note= "Kringle 4 - Figure 3"
 US-08-763-328A-5

Query Match Score 417; DB 2; Length 78;
 Best Local Similarity 85.9%; Pred. No. 3.1e-40;
 Matches 67; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 RESULT 4
 US-09-066-028-23
 Sequence 23, Application US/09066028
 Patent No. 6024688
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 O'Reilly, Michael
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K4

US-09-335-525-23

Query Match 79.7%; Score 417; DB 4; Length 78;
Best Local Similarity 85.9%; Pred. No. 3.1e-40;
Matches 67; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 CYHNGOSYRGTFSTUTYGRTCOSWSSMMTPHRHORTPEYNPNDGLTMYCNRNPDAKGFW 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 CYHGDQSYGTSSTTIGKQCOSWSSMMTPHRHOKTPENYPNAGLTNYCNRNPDAKGFW 60

RESULT 6

US-08-612-788-22

Sequence 22, Application US/08612788
; Patent No. 5837612

GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769

NUMBER OF SEQUENCES: 45

TITLE OF INVENTION: Angiostatin Fragments and Method of Use

GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/7335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: Q5213-0126

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 22:

SEQUENCING CHARACTERISTICS:

LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Murine
IMMEDIATE SOURCE:
CLONE: K4

US-08-612-788-22

Query Match 70.6%; Score 369; DB 2; Length 78;
 Best Local Similarity 73.1%; Pred. No. 8.6e-35;
 Matches 57; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 Qy 64 CPTTDDPSIRWEYCNLTRC 81
 Db 61 CYTDDPSIRWEYCNLKRC 78

RESULT 8
 US-09-335-325-22
 ; Sequence 22, Application US/09335325
 ; Patent No. 6521439
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M., Judah O'Reilly, Michael Cao, Yihai Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/335,325
 ; FILING DATE: 17-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05213-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-3700
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 78 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Murine
 ; IMMEDIATE SOURCE:
 ; CLONE: K4
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 ; US-09-335-325-22

Query Match 70.6%; Score 369; DB 4; Length 78;
 Best Local Similarity 73.1%; Pred. No. 8.6e-35;
 Matches 57; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 Qy 64 CPTTDDPSIRWEYCNLTRC 81
 Db 61 CYTDDPSIRWEYCNLKRC 78

Query Match 70.6%; Score 369; DB 3; Length 78;
 Best Local Similarity 73.1%; Pred. No. 8.6e-35;
 Matches 57; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 Qy 64 CPTTDDPSIRWEYCNLTRC 81
 Db 61 CYTDDPSIRWEYCNLKRC 78

RESULT 9
 US-08-612-788-17
 Sequence 17, Application US/088612788
 Patent No. 5,837,682
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Micheal
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 CLASSIFICATION:
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORGANISM: Murine
 ORIGINAL SOURCE:
 IMMEDIATE SOURCE:
 CLONE: K3
 US-08-612-788-17

Query Match 59.8%; Score 313; DB 28; Length 78;
 Best Local Similarity 61.5%; Pred. No. 1.9e-21; Indels 0; Gaps 0;
 Matches 48; Conservative 9; Mismatches 21; Gaps 0;

QY 4 CYHNGSYRGTFSHTVGRTCOSWSMTPHRQRTOPENYPLGMNYCRNPDAUTGPW 63
 Db 1 CLKRGNRGNYRGTSTVSKRTCSRWEOTPHRNTPENFPCKNLENYCRNPDETAIW 60
 RESULT 11
 US-09-35-325-17
 Sequence 17, Application US/09335325
 Patent No. 6,024,688
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Micheal
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use

RESULT 10
 US-09-066-028-17
 Sequence 17, Application US/09066028
 Patent No. 6,024,688
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Micheal
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use

ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/335,325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIORITY DATA:
 APPLICATION NUMBER: US/08/335,325
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 TELEPHONE: 404-818-3700
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3799
 TELEX/FAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Murine
 IMMEDIATE SOURCE:
 CLONE: K3
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-335-325-17
 Query Match 59 88; Score 313; DB 4; Length 78;
 Best Local Similarity 61.5%; Pred. No. 1.9e-28;
 Matches 48; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
 RESULT 12
 US-08-612-788-20
 Sequence 20, Application US/08612788
 Patent No. 5837682
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-18-7700
 TELEFAX: 404-818-3729
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Porcine
 IMMEDIATE SOURCE:
 CLONE: K3
 US-09-066-028-20

Query Match 57.28; Score 299; DB 3; Length 78;
 Best Local Similarity 56.4%; Pred. No. 7.4e-27;
 Matches 44; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 4 CYHGNQSYRGTFESTVGRTCQWSMTPHRQRTPEVNPNGLTMYCRNPDAADGPW 63
 Db 1 CLKGRGENRGTGVTAGHICQRWAQSFHKHTRPNCPKNLLENCRNPGETAPW 60

RESULT 15
 US-08-612-788-18
 Sequence 18, Application US/08612788
 Patent No. 5,837,682

GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 O'Reilly, Michael
 Cao, Yihai
 Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335,325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 3,714
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-918-3700
 TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids

IMMEDIATE SOURCE:						
	CLONE:	R3	US-08-612-788-18			
QY	Query Match	54.5%	Score 285; DB 2;	Length 78;		
Db	Best Local Similarity	55.1%	Pred. No. 2.8e-25;			
QY	Matches	43; Conservative	10; Mismatches	25; Indels	0; Gaps	0;
Db						
QY	4	CYHGNGOSYRGTFSTTYGRTCCGSWSSMTPHRQRTPENYPNDGLTKNYCRNPDAADGPW 63				
Db	1	CKKGTEGNRGNVAVTSGHICQHWSAQTPTHNKTPENFPSKNLDENYCRNPDGKRAPW 60				
QY	64	CTTDDSDIRAEYCNETRC 81				
Db	61	CHTTNSCWRWZCKIPSC 78				

search completed: September 29, 2003, 08:37:06
Job time : 29 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:35:54 ; Search time 61 Seconds

(without alignments)
 220.760 Million cell updates/sec

Title: US-10-088-548-6

Perfect score: 523

Sequence: 1 VRQCYHNGQSRYGTFSTTVV.....SURVEYCNLTRCSSTEGTVV

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters:

201696

Minimum DB seq length: 0

Maximum DB seq length: 89

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:^{*}

```

1: /cgn2_6/ptodata/1/pubpaas/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaas/US06_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaas/US06_NEW_PUB.com:*
4: /cgn2_6/ptodata/1/pubpaas/US07_NEW_PUB.com:*
5: /cgn2_6/ptodata/1/pubpaas/PC07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaas/PC07_NEW_PUB.com:*
7: /cgn2_6/ptodata/1/pubpaas/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaas/US08_NEW_PUB.com:*
9: /cgn2_6/ptodata/1/pubpaas/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaas/US09_NEW_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaas/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaas/US09C_NEW_PUB.com:*
13: /cgn2_6/ptodata/1/pubpaas/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaas/US10_NEW_PUB.com:*
15: /cgn2_6/ptodata/1/pubpaas/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaas/US10_NEW_PUB.com:*
17: /cgn2_6/ptodata/1/pubpaas/US60_NEW_PUB.com:*
18: /cgn2_6/ptodata/1/pubpaas/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed,

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	417	79.7	78	9	US-09-753-064-5
2	417	79.7	78	9	US-09-761-120-23
3	417	79.7	78	10	US-09-335-325-23
4	417	79.7	78	12	US-10-267-137-9
5	417	79.7	78	15	US-10-131-241-23
6	369	70.6	78	15	US-09-761-120-22
7	369	70.6	78	10	US-09-335-325-12
8	369	70.6	78	15	US-10-131-241-22
9	313	59.8	78	9	US-09-761-120-17
10	313	59.8	78	10	US-09-335-325-17
11	313	59.8	78	15	US-10-131-241-17
12	299	57.2	78	9	US-09-761-120-20
13	299	57.2	78	10	US-09-335-325-20
14	299	57.2	78	15	US-10-131-241-20
15	285	54.5	78	15	US-10-131-241-18

Sequence 18, Appl
 Sequence 19, Appl
 Sequence 19, Appl
 Sequence 19, Appl
 Sequence 4, Appl
 Sequence 18, Appl
 Sequence 21, Appl
 Sequence 21, Appl
 Sequence 21, Appl
 Sequence 16, Appl
 Sequence 16, Appl
 Sequence 16, Appl
 Sequence 12, Appl
 Sequence 15, Appl
 Sequence 21, Appl
 Sequence 15, Appl
 Sequence 15, Appl
 Sequence 9, Appl
 Sequence 9, Appl
 Sequence 9, Appl
 Sequence 2, Appl
 Sequence 15, Appl
 Sequence 8, Appl
 Sequence 8, Appl
 Sequence 7, Appl
 Sequence 8, Appl
 Sequence 9, Appl
 Sequence 9, Appl
 Sequence 13, Appl
 Sequence 13, Appl
 Sequence 14, Appl
 Sequence 14, Appl
 Sequence 8, Appl
 Sequence 8, Appl
 Sequence 7, Appl
 Sequence 8, Appl
 Sequence 10-131-241-15

RESULT 1

US-09-753-064-5

; Sequence 5, Application US/09753064

; Patent No. US2001016644A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yihai

; FOLKMAN, M. JUDAH

; TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jones & Askey, LLP

; STREET: 191 Peachtree Street, 37th Floor

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: US

; ZIP: 30303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/753,064

; FILING DATE: 29-Dec-2000

; CLASSIFICATION DATA: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/763,528

; FILING DATE: 12-Dec-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren, William L.

; REGISTRATION NUMBER: 36,714

; REFERENCE/DOCKET NUMBER: 05940-0251

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-318-3700

; TELEFAX: 404-818-3795

; INFORMATION FOR SEQ ID NO: 5;

; SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..78
 OTHER INFORMATION: /note= "Kringle 4 - Figure 3"
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-753-064-5

Query Match Score: 417; DB: 9; Length: 78;
 Best Local Similarity: 85.9%; Pred. No.: 5..6e-39;
 Matches: 67; Conservative: 5; Mismatches: 6; Indels: 0; Gaps: 0;

QY 4 CYHGNQSYRGTFSTTYGRICQNSNSMTPHRQRTPEYPNPDGLTMYCRNPDADGPW 63
 Db 1 CYHGDQSYRGTSSTTGKRCQSMSMTPHRQKTFENYPNAGLTMYCRNPDADKGWP 60

QY 64 CFTTDPSIRWEYCNLTRC 81
 Db 61 CFTTDPSIRWEYCNLKC 78

RESULT 2
 US-09-761-120-23
 Sequence 23, Application US/09761120
 Patent No. US20020037847A1
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael
 TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
 FILE REFERENCE: 05940-0151 (43171-232068)
 CURRENT APPLICATION NUMBER: US/09/761,120
 CURRENT FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 09/309,821
 PRIOR FILING DATE: 1999-05-11
 PRIOR APPLICATION NUMBER: 08/866,735
 PRIOR FILING DATE: 1997-05-30
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: PatentIN version 3.0
 SEQ ID NO: 23
 LENGTH: 78
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Kringle 4
 US-09-751-120-23

Query Match Score: 417; DB: 9; Length: 78;
 Best Local Similarity: 85.9%; Pred. No.: 5..6e-39;
 Matches: 67; Conservative: 5; Mismatches: 6; Indels: 0; Gaps: 0;

QY 4 CYHGNQSYRGTFSTTYGRICQNSNSMTPHRQRTPEYPNPDGLTMYCRNPDADGPW 63
 Db 1 CYHGDQSYRGTSSTTGKRCQSMSMTPHRQKTFENYPNAGLTMYCRNPDADKGWP 60

QY 64 CFTTDPSIRWEYCNLTRC 81
 Db 61 CFTTDPSIRWEYCNLKC 78

RESULT 4
 US-10-267-137-9
 Sequence 9, Application US/10267137
 Publication No. US20031489504A1
 GENERAL INFORMATION:
 APPLICANT: Xie, Li
 APPLICANT: Li, Zai-Ping
 APPLICANT: Gan, Ren-bao
 APPLICANT: Xu, Ren
 APPLICANT: Zou, Qing-wei
 TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCYTE
 TITLE OF INVENTION: GROWTH FACTOR AND USES THEREFOR

RESULT 3
 US-09-325-325-23
 Sequence 23, Application US/09335325
 Patent No. US2002016471A1
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah

FILE REFERENCE: 524282000100
; CURRENT APPLICATION NUMBER: US/10/267,137
; CURRENT FILING DATE: 2002-10-07
; PRIORITY NUMBER: 60/328,329
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence alignment of kringle domains of
; plasminogen and HGF
; US-10-267-137-9

Query Match 79.7%; Score: 417; DB: 12; Length: 78;
Best Local Similarity 85.9%; Pred. No. 5. 6e-39;
Matches 67; Conservative 5; Missmatches 6; Indels 0; Gaps 0;

QY 4 CYHNGQSYRGTTESTTYGRTQCSWSSMTPHRQTPENYPNDGLTMNYCRNPDAKGWP 63
|||||:|||||:|||||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 CYHNGQSYRGTTESTTYGRTQCSWSSMTPHRQTPENYPNDGLTMNYCRNPDAKGWP 60

QY 64 CFTTDPSPRWEICNLTRC 81
Db 61 CFTTDPSPRWEICNLKRC 78

RESULT 5
US-10-131-241-23
; Sequence 23, Application US/10131241
; Publication No. US2003001272A1

GENERAL INFORMATION:
; APPLICANT: Holdaway, John W.
; ATTORNEY: Fortier, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Regulating Angiogenesis Using Cancer Markers
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131,241
; CURRENT FILING DATE: 2000-07-22
; PRIORITY NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIORITY NUMBER: US 60/086,586
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 23
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-23

Query Match 79.7%; Score: 417; DB: 15; Length: 78;
Best Local Similarity 85.9%; Pred. No. 5. 6e-39;
Matches 67; Conservative 5; Missmatches 6; Indels 0; Gaps 0;

QY 4 CYHNGQSYRGTTESTTYGRTQCSWSSMTPHRQTPENYPNDGLTMNYCRNPDAKGWP 63
Db 1 CYHNGQSYRGTTESTTYGRTQCSWSSMTPHRQTPENYPNDGLTMNYCRNPDAKGWP 60

QY 64 CFTTDPSPRWEICNLTRC 81
Db 61 CFTTDPSPRWEICNLKRC 78

RESULT 6
US-10-161-120-22
; Sequence 22, Application US/09761120
; Patent No. US2002003784A1
; GENERAL INFORMATION:

LENGTH: 78 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Murine
 IMMEDIATE SOURCE:
 CLONE: K4
 SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-335-325-22

Query Match 70.6%; Score 369; DB 10; Length 78;
 Best Local Similarity 73.1%; Prod. No. 1.2e-33;
 Matches 57; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 4 CYHNGOSYRTGSTTYGRTGTCQSNSMTPHRORTPEVNPNDGTMNCRNPDAIGPWN 63
 Db 1 CYSQDGSYRTGSTSITGKQSNWAMPFHRHSKTPENFDAGLEMAYCRNDGDKGPW 60

Qy 64 CFTTDPSIRKEYCNTRC 81
 Db 61 CFTTDPSVRKEYCNKRC 78

RESULT 8
 US-10-131-241-22
 ; Sequence 22, Application US/10131241
 ; Publication No. US20030012792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holaday, John W.
 ; ATTORNEY: Fortier, Anne H.
 ; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
 ; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
 ; FILE REFERENCE: 05213-0344 43170-27565
 ; CURRENT APPLICATION NUMBER: 08/19/13,241
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR APPLICATION NUMBER: US 09/413,049
 ; PRIOR FILING DATE: 1999-10-06
 ; PRIOR APPLICATION NUMBER: US 09/316,802
 ; PRIOR FILING DATE: 1999-05-21
 ; PRIOR APPLICATION NUMBER: US 60/086,586
 ; PRIOR FILING DATE: 1998-05-22
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 22
 ; LENGTH: 78
 ; TYPE: PR
 ; ORGANISM: Murinae sp.

US-10-131-241-22

Query Match 70.6%; Score 369; DB 15; Length 78;
 Best Local Similarity 73.1%; Prod. No. 1.2e-33;
 Matches 57; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 4 CYHNGOSYRTGSTTYGRTGTCQSNSMTPHRORTPEVNPNDGTMNCRNPDAIGPWN 63
 Db 1 CYSQDGSYRTGSTSITGKQSNWAMPFHRHSKTPENFDAGLEMAYCRNDGDKGPW 60

Qy 64 CFTTDPSIRKEYCNTRC 81
 Db 61 CFTTDPSVRKEYCNKRC 78

RESULT 9
 US-09-761-120-17
 ; Sequence 17, Application US/09761120
 ; Patent No. US200307847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah

APPLICANT: O'Reilly, Michael
 ; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
 ; FILE REFERENCE: 05944-0151 (43171-25068)
 ; CURRENT APPLICATION NUMBER: US/09/761,120
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: 09/309,821
 ; PRIOR FILING DATE: 1997-05-30
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 17
 ; LENGTH: 78
 ; TYPE: PR
 ; ORGANISM: Murinae gen. sp.
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Kringle 3
 US-09-761-120-17

Query Match 59.8%; Score 313; DB 9; Length 78;
 Best Local Similarity 61.5%; Prod. No. 1.9e-27;
 Matches 48; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Qy 4 CYHNGOSYRTGSTTYGRTGTCQSNSMTPHRORTPEVNPNDGTMNCRNPDAIGPWN 63
 Db 1 CYSQDGSYRTGSTSITGKQSNWAMPFHRHSKTPENFDAGLEMAYCRNDGDKGPW 60

RESULT 10
 US-09-335-325-17
 ; Sequence 17, Application US/09335325
 ; Patent No. US2002016477A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; O'Reilly, Michael
 ; Cao, Yihai
 ; Shim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotostatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release # 1., Version # 1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/335,325
 ; FILING DATE: 17-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William D.
 ; REGISTRATION NUMBER: 05213-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-3799
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 78 amino acids

TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENS: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Murine
 IMMEDIATE SOURCE:
 CLONE: K3

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-335-325-17

Query Match 59.8%; Score: 313; DB: 10; Length: 78;
 Best Local Similarity 61.5%; Pred. No. 1.9e-27;
 Matches 48; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Qy 4 CYHNGQSYRTGTFSTTVGRTQCSWSSNTPHRHQRTPENPNPDGLTANYCRNPDAUTGPW 63
 Db 1 CLKGERGYRGTVSQTGTCRWSATPHHRNRPENPCKRLENYCRNPDETA PW 60

Query Match 57.2%; Score: 299; DB: 9; Length: 78;
 Best Local Similarity 56.4%; Pred. No. 6.9e-26;
 Matches 44; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
 FEATURE:
 NAME/KEY: misc_feature
 ORGANISM: Sus sp.
 OTHER INFORMATION: Kringle 3

US-09-761-120-20

Qy 4 CYHNGQSYRTGTFSTTVGRTQCSWSSNTPHRHQRTPENPNPDGLTANYCRNPDAUTGPW 63
 Db 1 CLKGERGYRGTVSQTGTCRWSATPHHRNRPENPCKRLENYCRNPDETA PW 60

Query Match 57.2%; Score: 299; DB: 9; Length: 78;
 Best Local Similarity 56.4%; Pred. No. 6.9e-26;
 Matches 44; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
 FEATURE:
 NAME/KEY: misc_feature
 ORGANISM: Sus sp.
 OTHER INFORMATION: Kringle 3

US-09-761-120-20

RESULT 11
 US-10-131-241-17
 Sequence 17, Application US/10131241
 Publication No. US20030012792A1
 GENERAL INFORMATION:
 APPLICANT: Holiday, John W.
 FORTIER, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
 FILE REFERENCE: 05213-0344 43170-271555
 CURRENT APPLICATION NUMBER: US/10/131,241
 CURRENT FILING DATE: 2002-07-22
 PRIOR APPLICATION NUMBER: US 09/413,049
 PRIOR FILING DATE: 1999-10-06
 PRIOR APPLICATION NUMBER: US 09/316,802
 PRIOR FILING DATE: 1999-05-21
 PRIOR APPLICATION NUMBER: US 60/086,586
 PRIOR FILING DATE: 1998-05-22
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 17
 LENGTH: 78
 TYPE: PRT
 ORGANISM: Murine
 US-10-131-241-17

Query Match 59.8%; Score: 313; DB: 15; Length: 78;
 Best Local Similarity 61.5%; Pred. No. 1.9e-27;
 Matches 48; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

Qy 4 CYHNGQSYRTGTFSTTVGRTQCSWSSNTPHRHQRTPENPNPDGLTANYCRNPDAUTGPW 63
 Db 1 CLKGERGYRGTVSQTGTCRWSATPHHRNRPENPCKRLENYCRNPDETA PW 60

Query Match 57.2%; Score: 299; DB: 9; Length: 78;
 Best Local Similarity 56.4%; Pred. No. 6.9e-26;
 Matches 44; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
 FEATURE:
 NAME/KEY: misc_feature
 ORGANISM: Sus sp.
 OTHER INFORMATION: Kringle 3

US-09-761-120-20

Qy 4 CYHNGQSYRTGTFSTTVGRTQCSWSSNTPHRHQRTPENPNPDGLTANYCRNPDAUTGPW 63
 Db 1 CLKGERGYRGTVSQTGTCRWSATPHHRNRPENPCKRLENYCRNPDETA PW 60

Query Match 57.2%; Score: 299; DB: 9; Length: 78;
 Best Local Similarity 56.4%; Pred. No. 6.9e-26;
 Matches 44; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
 FEATURE:
 NAME/KEY: misc_feature
 ORGANISM: Sus sp.
 OTHER INFORMATION: Kringle 3

US-09-761-120-20

RESULT 12
 US-09-61-120-20
 Sequence 20, Application US/09761120
 Patent No. US20020037847A1
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Parentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335/325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 78 amino acids
 TYPE: amino acid

STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Porcine
 IMMEDIATE SOURCE:
 CLONE: K3
 SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 US-09-335-325-20

Query Match	57.2%	Score 299;	DB 10;	Length 78;
Best Local Similarity	56.4%;	Pred. No.	6.9e-26;	
Matches	44;	Mismatches	22;	Indels 0;
				Gaps 0;

Qy 4 CYHNGQSYRGTFSSTVYGRFCQSNSMTPHRHQTENPNDGLTMCRNPDADGPW 63
 Db 1 CLKGGENTRGTIVSNTASGHTCQRMSAQSPHKHNRTEPNFCKNLDENYCRNPDGETAPW 60

Qy 64 CFTTDPSTIWEYCNLTC 81
 Db 61 CYTTDSEVRWDYCKIPSC 78

RESULT 14
 US-10-131-241-20
 Sequence 20, Application US/10131241
 Publication No. US20030012792A1
 GENERAL INFORMATION:
 APPLICANT: Holaday, John W.
 APPLICANT: Fortier, Anne H.
 TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Regulating Angiogenesis Using Cancer Markers
 FILE REFERENCE: 05213-034-43170-271565
 CURRENT FILING DATE: 2002-07-22
 PRIORITY NUMBER: US 09/413,049
 PRIORITY FILING DATE: 1999-10-06
 PRIOR APPLICATION NUMBER: US 10/131,241
 PRIORITY NUMBER: US 09/413,049
 PRIORITY FILING DATE: 1999-05-21
 PRIOR APPLICATION NUMBER: US 60/086,586
 PRIORITY NUMBER: 1998-05-22
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 20
 LENGTH: 78
 TYPE: PRT
 ORGANISM: Porcine
 US-10-131-241-20

Query Match

Best Local Similarity	56.4%;	Pred. No.	6.9e-26;	Length 78;
Matches	44;	Mismatches	22;	Indels 0;
				Gaps 0;

Qy 4 CYHNGQSYRGTFSSTVYGRFCQSNSMTPHRHQTENPNDGLTMCRNPDADGPW 63
 Db 1 CLKGGENTRGTIVSNTASGHTCQRMSAQSPHKHNRTEPNFCKNLDENYCRNPDGETAPW 60

Qy 64 CFTTDPSTIWEYCNLTC 81
 Db 61 CYTTDSEVRWDYCKIPSC 78

RESULT 15
 US-09-335-325-18
 Sequence 18, Application US/09335325
 Patient No. US20030164717A1
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 O'Reilly, Michael
 Cao, Yihai

Search completed: September 29, 2003, 08:45:29
 Job time : 62 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:30:58 ; Search time 39 Seconds
(without alignments)
219.462 Million cell updates/sec

Title: US-10-088-548-6
Perfect score: 523
Sequence: 1 VRQCYHGRNQSPRGTFSTTV.....SIRWEYCNLTCRCSDETEGVV 89

Scoring table: BLASTM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 30955

Minimum DB seq length: 0

Maximum DB seq length: 89

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	354	67.7	89 2 A60140	Plasmin (EC 3.4.21.21)
2	64	12.2	64 1 JX0060	short neurotoxin - short neurotoxin -
3	61.5	11.8	61 1 NLR12	1g kappa chain -
4	54	10.3	67 2 S2216	hypothetical protein
5	52	9.9	76 2 T31687	intestinal trefoil
6	52	9.9	81 2 A41441	kappa-3 neurotoxin
7	50	9.6	87 2 B60549	proteinase inhibitor
8	49.5	9.5	77 2 T14395	hypothetical protein
9	49.5	9.5	88 2 S41030	H ⁺ -transporting tw
10	49	9.4	55 2 E58892	capsid gene 5'-reg
11	49	9.4	82 2 S23703	high-potential iron
12	48	9.2	72 2 SA1611	conserved hypothetical
13	48	9.2	81 2 AC0142	PS2 protein precursor
14	47.5	9.1	84 2 A2666	hypothetical protein
15	47.5	9.1	85 2 G65176	short neurotoxin 1
16	47	9.0	60 1 NIEY1	NADH dehydrogenase
17	46.5	8.9	79 2 T11380	hypothetical protein
18	46	8.9	73 2 AF0060	protein T2205_7 (Ii
19	46	8.8	77 2 D84401	hypothetical protein
20	46	8.8	77 2 T14393	intestinal trefoil
21	46	8.8	80 2 S23963	protease inhibitor
22	45.5	8.7	77 2 S30578	hypothetical protein
23	45	8.6	52 2 S63324	mambin - eastern J
24	45	8.6	59 1 T6EP5J	short neurotoxin 1
25	45	8.6	60 1 NIAT1	short neurotoxin 1
26	45	8.6	60 1 NIATP	hypothetical protein
27	45	8.6	60 2 A27580	envelope protein -
28	45	8.6	64 2 E87477	
29	45	8.6	77 2 S35815	

ALIGNMENTS

RESULT 1						
A60140	plasmin (EC 3.4.21.7) precursor - chicken (fragment)					
N;Alternate names: plasminogen						
C;Species: Gallus gallus (chicken)						
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999						
C;Accession: A60140						
R;Greens, M.; Pattay, L.						
BioChim. Biophys. Acta 832, 326-330, 1985						
A;Title: The kringle 4 domain of chicken plasminogen.						
A;Reference number: A60140; PMID:8607796; PMID:4074753						
A;Accession: A60140						
A;Molecule type: protein						
A;Residues: 1-89 <PRE>						
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homo-						
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase;						
F;6-83-27-66-55-78/Disulfide bonds: #status Predicted						
F;39/Binding site: carbohydrate (Asn) (covalent) #status Experimental						
Query Match Score: 67.7%; Best Local Similarity: 67.9%; Best Matches: 55;保守性: 11; Mismatches: 15; Indels: 0; Gaps: 0;						
Query Match Score: 67.7%; Best Local Similarity: 67.9%; Pred. No. 2, 1e-29; Best Matches: 55;保守性: 11; Mismatches: 15; Indels: 0; Gaps: 0;						
QY 3 QCYHGNQSYRGTFSYTFGTCQWSMTPHQRPEPNPDOLTMYCRNPDAADGP 62						
Dd 5 ECYQGQGVSRGTFASFTTGKRCQAWNSMSPHRNKTESHPNADLRQNYCRNPDAADSP 64						
QY 63 WCFTRDTPSITRWEYCNLFRCSD 83						
Db 65 WCYTTDDPSYRWEYCNLKRCSD 85						

RESULT 2						
C;Species: Bungarus fasciatus (banded krait)						
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993						
C;Accession: JX0060						
C;R;Liu, C.S.; Chen, J.P.; Chang, C.S.; Lo, T.B.						
C;J. Biochem. 105, 93-97, 1989						
A;Title: Amino acid sequence of a short chain neurotoxin from the venom of banded krait						
A;Reference number: JX0060; PMID:86291813; PMID:2738048						
A;Accession: JX0060						
A;Molecule type: protein						
A;Residues: 1-64 <END>						
C;Superfamily: snake toxin						
C;Keywords: postsynaptic neurotoxin						
Query Match Score: 12.2%; Best Local Similarity: 26.7%; Pred. No. 7, 2; Best Matches: 16; Conservative: 7; Mismatches: 27; Indels: 10; Gaps: 1;						

A;Accession: T34687
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-76 <HAR>
A;Cross-references: EMBL:AL023517; PIDN:CAA18983..1; GSPDB:GN00070; SCOEDB:SC1B5..09c
A;Experimental source: strain A3 (2)
C;Genetics:
A;Gene: SCOEDB:SC1B5..09c

RESULT 3
N1R12
short neurotoxin 2 - ringhals
N;Alternate names: neurotoxin IV
C;Species: *Haemachatus haemachatus*, Sepedon haemachatus (ringhals)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C;Accession: A01701
R;Birol, A.; Botes, D.P.
J;Birol, Chem. 246, 1341-1349, 1971
A;Title: Snake venom toxins: Purification, properties, and complete amino acid sequence
A;Reference number: A92073; MUID:7116407; PMID:5545078
A;Accession: A01701
A;Molecule type: protein
A;Residues: 1-61 <SPR>
C;Superfamily: snake toxin
C;Keywords: neurotoxin; venom
F;3-3,17-40,42-53,54-59/disulfide bonds: #status predicted

Query Match Score 11.8%; DB 1; Length 61;
Best Local Similarity 26.18%; Pred. No. 12;
Matches 23; Conservative 8; Mismatches 20; Indels 37; Gaps 5;

QY 3 QCYHGNQSYRGTSSTTYGRNC-----QSRSSTMPHRQHTPENYFNDGLTNNCR 54
Db 2 ECH- -RQS-----SQTPTQPGTCNYKKKNSD-- -HRGSRT----- 36

QY 55 NPPADFGPWCTTDSEIWEYNLIRCS 82
Db 37 -----ERGGCGPTVKFGIKLKCCCTDDRCN 60

RESULT 4
S24.2.16
19 kappa chain - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24216
R;Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1055-1072, 1991.
A;Title: Deletions of immunoglobulin C (kappa) region characterized by the circular excis
A;Reference number: S24214; MUID:91217618; PMID:1902500
A;Molecule type: DNA
A;Residues: 1-67 <SH1>
A;Cross-references: EMBL:X58221; NID:953719; PIDN:CAA41185..1; PID:9530196
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match Score 10.3%; DB 2; Length 67;
Best Local Similarity 39.5%; Pred. No. 80;
Matches 15; Conservative 1; Mismatches 18; Indels 4; Gaps 1;

RESULT 5
T34687
hypothetical protein SC1B5..09c SC1B5..09c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T34687
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, May 1998
A;Reference number: 221553

QY 1 VRQCYHGNQSYRGTS-----TIVTGRICOSWSSMTPH 34
Db 20 VRFGSGSGTSTLISMEAEDAAVYCQWSSYPPH 57

RESULT 6
A41441
intestinal trefoil factor precursor - rat
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Jul-1999
C;Accession: A41441
R;Sueno, S.; Lynch-Deraney, K.; Podolsky, D.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 11017-11021, 1991
A;Title: Identification and characterization of rat intestinal trefoil factor: tissue
A;Reference number: A41441; MUID:92107881; PMID:1763017
A;Accession: A41441
A;Molecule type: mRNA
A;Residues: 1-81 <SPR>
A;Cross-references: GB:ME80826; PIDN:AAA42270..1; PID:g207447
C;Superfamily: secretory protein xPL; trefoil homology
C;Keywords: intestine

QY 34 HRHQRTPEPNYFNDGLTM-----RNPDADTGWC 68
Db 5 HGHDREE--PDAGCEPGGYCLIDAPRPFKAQGPPFACYQCREPTEPESYKGITLC 61

QY 69 PSIRWEYCNLTRCS 82
Db 62 PYCEWQDAQRFTACS 75

RESULT 7
E360549
kappa-3 neurotoxin precursor - many-banded krait
N;Alternate names: kappa-3 bungarotoxin; kappa-neurotoxin CRI
C;Species: *Bungarus multicinctus* (many-banded krait)
C;Date: 17-Apr-1993 #sequence_revision 18-Jun-1993 #text_change 17-Mar-2000
C;Accession: S08398; B60349
R;Danse, J.M.; Garnier, J.M.
Nucleic Acids Res. 18, 1050, 1990
A;Title: cDNA deduced amino-acid sequences of two novel kappa-neurotoxins from Bungar
A;Reference number: S08398; MUID:90192091; PMID:2315018
A;Accession: S08398
A;Molecule type: mRNA
A;Residues: 1-87 <DAN>
A;Cross-references: EMBL:X51413; NID:962481; PIDN:CAA35775..1; PID:g62482

RiChiappinelli, V.A.; Wolf, K.M.; Grant, G.A.; Chen, S.J.
 Brain Res. 509, 237-248, 1990
 A;Title: Kappa-2-bungarotoxin and kappa-3-bungarotoxin: two new neuronal nicotinic receptors
 A;Reference number: A60549; MUID:90213167; PMID:2322821
 A;Accession: B60549
 A;Molecule type: protein
 A;Residues: 22-66 <CHD>
 C;Comment: Kappa-3 neurotoxin exists as homodimers and as heterodimers with kappa-2-neuroneurotoxin; homodimer; neurotoxin
 C;Keywords: heterodimer; homodimer; neurotoxin
 F;1-21;Domain: signal sequence #status predicted <SIG>
 F;22-87;Product: kappa-3-neurotoxin #status experimental <MAT>

Query Match 9.6%; Score: 50; DB: 2; Length: 87;
 Best Local Similarity: 29.4%; Pred. No. 2.7e+02;
 Matches: 20; Conservative: 6; Mismatches: 24; Indels: 18; Gaps: 5;

QY 23 RTCQSNSSMTPHRHQROPENPN-----DGITMNNC--RNPDAADGPWCYTDESTRW 73
 Db 22 RTC----LISP-----SSPOTCPNGGDCIFRKACDNCHSRGPVTEOG--CVATCFCFRS 72

QY 74 EYCNTRTC 81
 Db 73 NYRSLLCC 80

RESULT 8
 Proteinase inhibitor II - turnip
 C;Species: Brassica rapa (turnip)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
 C;Accession: M14395
 R;Kim, J.B.; Kim, H.U.; Yun, C.H.; Park, B.S.; Cho, W.S.; Ryu, J.C.; Chung, T.Y.
 Submitted to the EMBL Data Library, March 1996
 A;Description: Nucleotide sequences of protease inhibitor II in chinese cabbage.
 A;Reference number: Z18029
 A;Accession: M14395
 A;Status: preliminary; translated from GB/EMBL/DBBJ
 A;Molecule type: mRNA
 A;Residues: 1-77 <KTM>
 A;Cross-references: EMBL:L11937; NID:91209257; PID:g1209258
 A;Experimental source: unopened flower bud
 C;Superfamily: gamma-thionin

Query Match 9.5%; Score: 49.5%; DB: 2; Length: 77;
 Best Local Similarity: 38.1%; Pred. No. 2.7e+02;
 Matches: 16; Conservative: 3; Mismatches: 16; Indels: 7; Gaps: 2;

QY 14 GTFTSTVIGRTQCSWSSMTPHRHQPENTPNDDLTNYCRN 55
 Db 22 GMGPVTVEARTECKS---HAFKGICVSTTNCO---NVCHN 56

RESULT 9
 hypothetical protein K03HL.7 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
 C;Accession: S41030
 R;Smith, M.; Ainscough, R.
 submitted to the EMBL Data Library, January 1994
 A;Reference number: S41024
 A;Accession: S41030
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-88 <SM>
 A;Cross-references: EMBL:Z29560; NID:9450886; PID:g450893
 C;Genetics:
 A;Introns: 47/2; 87/1

Query Match 9.5%; Score: 49.5%; DB: 2; Length: 88;
 Best Local Similarity: 29.4%; Pred. No. 3e+02;
 Matches: 15; Conservative: 7; Mismatches: 14; Indels: 15; Gaps: 2;

RESULT 15
 G69176 hypothetical protein MTH58 - Methanobacterium thermoautotrophicum (strain Delta H)
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C;Accession: G69176
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 i; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J.; Bacteriol., 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A;Reference number: A69000; PMID:98037514; PMID:3371463
 A;Accession: G69176
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-85 <MTH>
 A;Cross-references: GB:AE000798; GB:AE000666; NID:92621094; PID:9262109
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH58

Query Match 9.1%; Score 47.5; DB 2; Length 85;
 Best Local Similarity 25.0%; Pred. No. 4.7e-02;
 Matches 19; Conservative 12; Mismatches 26; indels 19; Gaps 4;
 QY 18 TTYNGRGTQCSWSSMPHRIORTPEN--YPNDGLIMNYCRNPD-ADGPGCETTDPISRW 73
 8 TGIGK-----QRPVIDGVVYPEDSYTIVETWKPGMLEGP--YTARTEKRY 52
 QY 74 EYCNLTRCSDTPGTVV 89
 Db 53 GRFHQTKELETSDDTVI 68

Search completed: September 29, 2003, 08:36:31
 Job time : 41 secs

4 protein - protein search, using sw model						
Run on:		September 29, 2003, 08:23:28 ; Search time 23 Seconds (without alignments) 181.973 Million cell updates/sec				
title:	US-10-088-548-6					
perfect score:	523					
sequence:	1.VRQCYHGNQSYRGTFSSTVV.....SIRWEYCNLTROSDEGGTVV	89				
scoring table:	BLOSUM62					
gapopen:	Gap0 10.0 , Gapext 0.5					
searched:	127863 seqs, 4702605 residues	11264				
total number of hits satisfying chosen parameters:						
minimum DB seq length:	0					
maximum DB seq length:	89					
post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
database :	SwissProt_41;*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
result No.	Score	Query Match	Length	DB ID	Description	
1	64	12.2	64	1 NSKL_BUNFA	P10808 bungarus m	
2	61.5	11.8	61	1 NX52_HERMHA	P01433 hemachatus	
3	50.5	9.7	81	1 POC3_STIRU	P58111 syringurus	
4	50.5	9.7	84	1 POC3_OLEBU	081092 olea europaea	
5	50.0	9.6	87	1 NX53_BUNMU	P15711 bungarus m	
6	49	9.4	55	1 ATP8_LATCH	P03168 latimeria	
7	48	9.2	72	1 HP11_ECTVA	P38945 ectothiorhynchus	
8	47.5	9.1	84	1 TFEFL_HUMAN	P04155 homo sapiens	
9	47	9.0	60	1 NX51_ENHSC	P25432 erythrina	
10	46	8.8	81	1 TFP3_RAT	P03119 rattus norvegicus	
11	45.5	8.7	37	1 SCFTI_NESTA	P81761 mesobuthus	
12	45.5	8.7	77	1 THC1_ARATH	P39182 sphaerocaryum	
13	45	8.6	52	1 YNF8_YEAST	P53820 dendroaspis	
14	45	8.6	59	1 MAMB_DENJUA	P01438 astrotia	
15	45	8.6	60	1 NX51_ASPST	P25677 naja haje	
16	45	8.6	60	1 TXPA_NAJHA	P25678 naja haje	
17	45	8.6	61	1 TXPA_NAJHA	P04201 rattus norvegicus	
18	45	8.6	70	1 CPTX2_RAT	P01398 bungarus m	
19	45	8.6	87	1 NX51_BONMU	P36223 ornithodoros	
20	44.5	8.5	60	1 DIESG_ORNMO	P10457 laticauda	
21	44.5	8.5	62	1 NX52_LATCO	P25495 laticauda	
22	44.5	8.5	62	1 NX5A_LATCR	P01425 hemachatus	
23	44	8.4	61	1 NX51_HERMHA	P15227 buthus siro	
24	44	8.4	88	1 RI134_MEETH	P32879 aibysurus	
25	43.5	8.3	62	1 NX5C_LATCR	P19958 aipysurus	
26	43.5	8.3	77	1 THG2_ARATH	P04194 arabidopsis	
27	43.5	8.3	62	1 CXAB_CONWR	P26443 conus marmoratus	
28	43.5	8.3	86	1 TXP2_NAJAT	P09417 naja atra	
29	43	8.2	35	1 SCX1_BUTSI	P15226 buthus siro	
30	43	8.2	60	1 NYSL_AIPLA	P19958 aipysurus	
31	43	8.2	60	1 NX52_AIPLA	P28040 mesobuthus	
32	43	8.2	60	1 SCX3_MERSTA	P09052 scincellus	
33	42	8.2	65	1 VSP1_BUTSI	P15227 buthus siro	

Best Local Similarity 30.2%; Pred. No. 62; Mismatches 13; Conservative 6; Indels 21; Gaps 3; 1;

QY 5 YHGGNGSYRGITSTTGYGRCQSWSMTPHRHQRTPEYNPDG 47
Db 18 FDANGD---GKISSSELGEFLKLIGSVTFEEIQRMMAEIDTDG 57

RESULT 5
NXL3_BUINMU

ID NXL3_BUINMU STANDARD; PRT; 87 AA.

AC P15817; P87353;

DT 01-APR-1990 (Rel. 14, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Long neurotoxin CRI precursor (kappa neurotoxin) (Kappa3-Bungarotoxin).

DE Bungarotoxin multicinctus (Many-banded krait).

OS Elapsoidea; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Bungarinae; Bungars.

OC NCBITaxID=8816;

OX NCBI_TaxID=8816;

RN SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RX MEDLINE=30192091; PubMed=2315018;

RA Danse J.M.; Garnier J.M.;

RT "cDNA deduced amino-acid sequences of two novel kappa-neurotoxins from Bungarus multicinctus";
Nucleic Acids Res. 18:1050-1050(1990).

RN [2]

RP SEQUENCE FROM N.A.

RA Chang L.-S.; Lin J.-J.; Hong E.-i.

RT "The exon-intron structure of kappa3-bungarotoxin precursor from Taiwan banded krait.";
Submitted (MR-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: NEUROTOXIN BINDS AND INHIBITS NICOTINIC RECEPTORS COMPARED TO ALPHA-NEUROTOXINS, KAPPA-NEUROTOXIN BIND MORE STRONGLY TO NEURONAL RECEPTORS, AND LESS STRONGLY TO MUSCLE RECEPTORS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- SIMILARITY: Belongs to the snake toxin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; U82228; P4AC60322; 1; -

CC DR PIR; E58892; E58892.

CC DR InterPro; IPR01421; AtPass8-mit.

CC DR Pfam; PF0095; ATP-synt_8_1;

CC KW Hydrogen ion transport; CF_0; Mitochondrion; Transmembrane.

CC FT TRANSMEM 4 24 POTENTIAL.

CC SQ SEQUENCE 55 AA; 6569 MW; TFE36519ESAF825B CRC64;

DR EMBL; X51413; CAA3575.1; -;

DR EMBL; Y11769; CAA12434.1; -;

DR PIR; S08398; B60549.

DR HSP; P01398; 1KBA.

DR InterPro; IPR003571; Snake_toxin.

DR Pfam; PF00087; toxin_1.

DR PROSITE; PS00272; SNAKE_TOXIN_1.

KW Toxin; Neurotoxin; Multigene family; Signal.

FT SIGNAL 1 21 LONG NEUROTOXIN CRL.

FT CHAIN 22 87 BY SIMILARITY.

FT DISULFID 24 42 BY SIMILARITY.

FT DISULFID 35 63 BY SIMILARITY.

FT DISULFID 48 52 BY SIMILARITY.

FT DISULFID 67 79 BY SIMILARITY.

FT DISULFID 80 85 BY SIMILARITY.

FT CONFLICT 7 7 S->T (IN REF. 2).

SQ SEQUENCE 87 AA; 9660 MW; A08AF400FFEBB66 CRC64;

Query Match 9.6%; Score 50; DB 1; Length 87;

Best Local Similarity 29.4%; Pred. No. 73; Mismatches 6; Indels 24; Gaps 5;

QY 23 RTCQSHSSMTPHRHQRTPEYNP----DGLTMNYC----RNPDAADGPGCPTTDPSIRW 73
Db 22 RTC---SSPQTCEPGNDICPRKAQCDNFCHSRGPVTEQG--CVATCPQFRS 72

RESULT 6
ATP8_LATCH

ID ATP8_LATCH STANDARD; PRT; 55 AA.

AC 003168;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).

DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).

GN MTARP8 OR ATP8

OS Latimeria chalumnae (Latimeria) (Coelacanth).

OC Eukaryota; Metzoza; Chordata; Craniata; Vertebrata; Buteleostomi; Coelacanthiformes; Coelacanthidae; Latimeria.

OC NCBI_TaxID=7897;

OX NCBI_TaxID=7897;

RN RN

RP SEQUENCE FROM N.A.

RA Zardoya R.; Meyer A.;

RL Submitted (DEC 1996) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMIC COMPONENT (CF(0)) SUBUNIT OF THE MITOCHONDRIAL ATPASE COMPLEX.

CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).

CC -!- SUBCELLULAR LOCATION: Membrane-bound.

CC -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; U82228; P4AC60322; 1; -

CC DR InterPro; IPR01421; AtPass8-mit.

CC DR Pfam; PF0095; ATP-synt_8_1;

CC KW Hydrogen ion transport; CF_0; Mitochondrion; Transmembrane.

CC FT TRANSMEM 4 24 POTENTIAL.

CC SQ SEQUENCE 55 AA; 6569 MW; TFE36519ESAF825B CRC64;

DR EMBL; X51413; CAA3575.1; -;

DR EMBL; Y11769; CAA12434.1; -;

DR PIR; S08398; B60549.

DR HSP; P01398; 1KBA.

DR InterPro; IPR003571; Snake_toxin.

DR Pfam; PF00087; toxin_1.

DR PROSITE; PS00272; SNAKE_TOXIN_1.

KW Toxin; Neurotoxin; Multigene family; Signal.

FT SIGNAL 1 21 LONG NEUROTOXIN CRL.

FT CHAIN 22 87 BY SIMILARITY.

FT DISULFID 24 42 BY SIMILARITY.

FT DISULFID 35 63 BY SIMILARITY.

FT DISULFID 48 52 BY SIMILARITY.

FT DISULFID 67 79 BY SIMILARITY.

FT DISULFID 80 85 BY SIMILARITY.

FT CONFLICT 7 7 S->T (IN REF. 2).

SQ SEQUENCE 87 AA; 9660 MW; A08AF400FFEBB66 CRC64;

Query Match 9.6%; Score 50; DB 1; Length 87;

Best Local Similarity 29.4%; Pred. No. 73; Mismatches 6; Indels 24; Gaps 5;

CC 3;

QY 27 SR---SSMTHPRHTPEYNPDGTMNYC-RNPDAADGPGW 63
Db 16 SM1FLIMPLSKTL--HTFPNNPSTQNMCKQEPEPWTPW 54

RESULT 7
HP1_ECTVA

ID HP1_ECTVA STANDARD; PRT; 72 AA.

AC P38941;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE High Potential iron-sulfur protein isozyme 1 (HIPIP 1).

GN HIPIP

OS Ectothiorhodospira vacuolata.

OC Bacteria; Protoplasts; Gammaproteobacteria; Chromatiales; Ectothiorhodospiraceae; Ectothiorhodospira.

OC NCBITaxID=1054;

- [1] RN SPOUSEN-Beta-1 / DSM 2111; RP SEQUENCE FROM N.A. RT "Structure of the human oestrogen-responsive gene PS2." ; RL Nucleic Acids Res. 15:1401-1414(1987). [4]

[2] RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RT MEDLINE=90236983; PubMed=215238; RX Mori K., Fujii R., Kida N., Takahashi H., Ohkubo S., Fujino M., Ohta M., Hayashi K.; RT "Complete primary structure of the human estrogen-responsive gene (PS2) product." ; RT J. Biochem. 107:73-76(1990). [5]

[3] RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RT MEDLINE=90184461; PubMed=2311759; RX Takahashi H., Kida N., Fujii R., Tanaka K.I., Ohta N., Mori K., Hayashi K.; RT "Expression of the PS2 gene in human gastric cancer cells derived from poorly differentiated adenocarcinoma." ; RT FEBS Lett. 261:283-286(1990). [6]

[4] RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RT MEDLINE=20408883; PubMed=10950923; RX Berry A., Scott H.S., Kudoh J., Taylor I., Korostishevsky M., Wittenhofer M., Guillepin M., Barras C., Rossier C., Shibusawa K., Park H.-S., Toyota A., Ishii K., Totoki Y., Choi D.-K., Groner Y., Soeda E., Okhi M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Antonarakis S., Bonne-Tamir B.; RT "Refined localization of autosomal recessive nonsyndromic deafness DFNB10 locus using 34 novel microsatellite markers, genomic structure, and exclusion of six known genes in the region." ; RT Genomics 68:22-29(2000). [7]

[5] RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RT MEDLINE=20289799; PubMed=10830953; RX Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Horikoshi K., Yamamoto K., Matsuyama S., Shimizu N., Antonarakis S.E., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwiedl K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Nagai T., Nagardine G., Nordstiek G., Antonarakis S.E., Minoshima S., Shimizu N., Nordstiek G., Antonarakis S.E., Wehrmeier S., Borzym K., Gardiner K., Riessmann L., Dägand E., Lehrach H., Reinhardt R., Yaspo M.-L., Francis F., RT "True DNA sequence of human chromosome 21." ; RT Nature 405:311-319(2000). [8]

[6] RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RT TISSUE-Colon, Kidney, and Stomach; RX STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shevchenko A.M., Schaefer C.F., Blitschul S.F., Zeeberg B.R., Buetow K.H., Bhattacharyya N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Soares M.B., Bonaldo M.F., Casavant T.L., Carninci P., Prange C., Brownstein M.J., Urdin T.B., Yoshihara S., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., McKernan K.J., Malek J.A., Bosak S.A., McElwan P.J., Hale S., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Bouffard G.G., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fakay J., Helton E., Kettenbach M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko I.Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grumwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Stalska U., Garnier J.M., Brown A.M.C., Schniech A., Schein J.E., Jones S.J.M., Mairra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." ; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [9]

DR EMBL: AB038162; BAB13729.1; - .
DR EMBL: AP001746; BA95532.1; - .
DR EMBL: BC032811; AAU32811.1; - .
DR PIR: A26667; A26667. - .
DR PDB: 1PS2; 07-TUL-07. - .
DR PDB: 1H17; 09-APR-01. - .
DR Genew; HGNC:11755; TFF1. - .
DR MIM; 113710. - .
DR GO; GO:0005975; P:carbohydrate metabolism; TAS. - .
DR GO; GO:008151; P:cell growth and/or maintenance; TAS. - .
DR InterPro; IPR000511; P:trefoil. - .
DR Pfam; PF00088; trefoil; 1. - .
DR PRINTS; PRO0680; FIREFOIL. - .
DR SMART; SM00018; PD. - .
DR PROSITE; PS00025; P_TREFOIL; 1. - .
DR Growth factor; Signal; Disease mutation; 3D-structure. - .
DR KW - .
DR SIGNAL; 1 24 - .
FT FT CHAIN 25 84 TREFOIL FACTOR 1. - .
FT FT DOMAIN 30 71 P-TYPE. - .
FT FT DISULFID 31 57 BY SIMILARITY. - .
FT FT DISULFID 41 56 BY SIMILARITY. - .
FT FT DISULFID 51 68 BY SIMILARITY. - .
Query Match 9.1%; Score 47.5; DB 1; Length 84; - .
Best Local Similarity 31.0%; Pred. No. 1.3e+02; - .
Matches 18; Conservative 6; Mismatches 19; Indels 15; Gaps 6 - .
QY 14 GFSTIVTGTTCQSSWMTPHRHQPENPNPDGTMNCRN----PDADTG-PWCDF 65 - .
Db 21 GTLAERQT-ETC---TVAPEQQNC-GFP-GVTPSQCANGGCCDDPTVGVWCF 69 - .

RESULT 9
NXS1_ENHSC STANDARD; PRT; 60 AA.

ID NX51_ENHSC_1; P01436; PRT; 60 AA.

AC P23492; P01436; PRT; 60 AA.

DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Short neurotoxin 1 (Toxin 4).

OS Enhydrina schistosa (Common sea snake), and
Lapemis hardwickii (Hardwick's sea snake).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Hydrophinae; Enhydrina.
NCBIXIID-8682, 8781; [1]

RN SEQUENCE,
RC SPECIES-E.schistosa; TISSUE-Venom;
RX MEDLINE-7312734; PubMed=4616045;
RA Fryklund L., Baker D., Karlsson E.;
RT "Amino acid sequences of the two principal neurotoxins of Enhydrina
schistosa venom.";
RL Biochemistry 11:4633-4640 (1972).
[2]
RP SEQUENCE,
RC SPECIES-E.hardwickii; TISSUE-Venom;
RX MEDLINE-7312734; PubMed=4616045;
RA Elzinga M., Tu A.T.;
RT hardwickii and the detection of a sulphydryl group by laser Raman
spectroscopy.";
RL FEBS Lett. 80:217-220 (1977).
CC -!
CC -!- FUNCTION: Produces peripheral paralysis by blocking neuromuscular
transmission at the postsynaptic site. Binds to the nicotinic
acetylcholine receptor.
CC -!
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MISCELLANEOUS: ID(50) IS 0.2 MG/KG BY INTRAVENOUS INJECTION FOR
CC -!- SIMILARITY: Belongs to the snake toxin family.
DR PIR; A01705; MEY1.
DR HSSP; P01426; 1NEA.

DR EMBL: X00474; CAA25155.1; - .
EMBL: X05030; CAZ28635.1; - .
EMBL: X05321; CAA28635.1; JOINED.
EMBL: X05322; CAA28635.1; JOINED.
EMBL: X05033; CAA36234.1; - .
EMBL: M12075; AAA52421.1; - .

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL curatorium - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: X00474; CAA25155.1; - .
EMBL: X05030; CAZ28635.1; - .
EMBL: X05321; CAA28635.1; JOINED.
EMBL: X05322; CAA28635.1; JOINED.
EMBL: X05033; CAA36234.1; - .
EMBL: M12075; AAA52421.1; - .

RESULT 11						
SCIT_MESTA	STANDARD;	PRT;	37 AA.			
ID PB1761; AC 28-FEB-2003 (Rel. 41, Created) DT 28-FEB-2003 (Rel. 41, Last sequence update)						
DT 28-FEB-2003 (Rel. 41, Last annotation update)						
DE Lepidopteran-selective toxin (Butait).						
OS Mesobuthus tamulus (Eastern Indian scorpion) (Buthus tamulus)						
QC Eukaryota; Metazoa; Arthropoda; Chelicerata; Scorpiones; Burhoidea; Butidae; Mesobuthus.						
OC NCBI_TAXID=34647;						
OX RN						
SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.						
TISSUE=venom;						
PubMed=11782289;						
RA Wadagiyar R., Inceoglu B., Herrmann R., Berbel M., Choudary P.V., Hammock B.D.;						
RC "Isolation and characterization of a novel lepidopteran-selective toxin from the venom of South Indian red scorpion, Mesobuthus tamulus," BMC Biochem. 2:16-16(2001).						
CC -1- FUNCTION: Induces flaccid paralysis in <i>H. virescens</i> larvae. Is not toxic to <i>S. fauvea</i> larvae or mice.						
CC -1- SUBCELLULAR LOCATION: Secreted.						
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.						
CC -1- MASS SPECTROMETRY: MW=3856.7; METHOD=Electrospray.						
CC -1- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY.						
GO: GO:0005576; C: extracellular; IDA.						
GO: GO:0019870; F: potassium channel inhibitor activity; NAS.						
DR GO:0005405; P: pathogenesis; IDA.						
DR GO: GO:0005405; P: pathogenesis; IDA.						
PFAM: PF005294; toxin_5; 1.						
KW Neurotoxin.						
FT DISULFID 2 19 BY SIMILARITY.						
FT DISULFID 5 27 BY SIMILARITY.						
FT DISULFID 16 32 BY SIMILARITY.						
FT DISULFID 20 34 BY SIMILARITY.						
SEQUENCE 37 AA; 3864 MW; FD36529E5F7CCD9 CRC64;						
Query Match 8.7%; Score 45.5%; DB 1; Length 37;						
Best Local Similarity 42.3%; Pref. No. 87;						
Matches 11; Conservative 3; Mismatches 5; Indels 7; Gaps						
QY 61 GPWCFTTDPDSIRWEYCNLTRCSDEG 86						
: :						
Db 3 GP-CFTTDPDQ-----AKCSECCG 21						
RESULT 12						
THGL_ARATH	STANDARD;	PRT;	77 AA.			
ID THGL_ARATH						
Q39182; AC 16-OCT-2001 (Rel. 40, Created)						
DT 16-OCT-2001 (Rel. 40, Last sequence update)						
DT 28-FEB-2003 (Rel. 41, Last annotation update)						
DE Gamma-thionin homolog At2g02100 precursor.						
GN AT2G02100 OR F504.13.						
OC Arabidopsis thaliana (mouse-ear cress).						
OC Spermatophyta; Magnoliophyta; Embryophyta; tracheophyta;						
OC eu dicots; core eudicots; Rosidae;						
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.						
OX NCBI_TAXID=3702;						
RN RP SEQUENCE FROM N.A.						
RC STRAIN=ev. C24; TISSUE=Flower buds;						
RC Yu D.Y., Quigley F., Mache R.;						
RT "Isolation and expression of a cDNA encoding protease inhibitor precursor."						
RT Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.						
RL [2]						
RN SEQUENCE FROM N.A.						
RC STRAIN=ev. Columbia;						

RESULT 13	
ID	YNT8_YEAST STANDARD; PRT; 52 AA.
AC	P53820; [Rel. 34, Created]
CP	01-OCT-1996 [Rel. 34, Last sequence update]
DP	01-OCT-1996 [Rel. 34, Last annotation update]
FT	DISULFID 44 BY SIMILARITY.
FT	DISULFID 50 BY SIMILARITY.
FT	DISULFID 54 BY SIMILARITY.
SEQUENCE	8324 MW; EC0466003610965 CRC64;
Query Match	8.7%; Score 45.5; DB 1; Length 77;
Best Local Similarity	35.7%; Pred. No. 1. 9e+02;
Matches	15; Mismatches 17; Indels 7; Gaps
24	14 GTESTINGTCGSSWMMTPHRQTHPENPNDGLTMNCRN 55
Ob	22 GMGPVTVARTCESQS -- HRFKGTCVSASN -- CANVCHN 56
RESULT 14	
ID	YNT8_YEAST STANDARD; PRT; 52 AA.
AC	P53820; [Rel. 34, Created]
CP	01-OCT-1996 [Rel. 34, Last sequence update]
DP	16-OCT-2001 [Rel. 40, Last annotation update]
FT	Hypothetical 6.0 kDa protein in COS1 S' region.
DN	YNL38W OR N1701.
DS	Saccharomyces cerevisiae (Baker's yeast).
DC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;
DC	Saccharomyctaceae; Saccharomyctidae; Saccharomyces.
NCBI_TAXID	4932; [Rel. 34, Last sequence update]
[1]	SEQUENCE FROM N.A.
OB	Obremer B.; Piravandi B.; Rinke M.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 CC -1- SIMILARITY: TO YEAST YHR217C.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR PIR; A42561; T65P5J.
 DR PDB; 1DPS; 20-DEC-94.

DR InterPro; IPR003571; Snake_toxin.

DR Pfam; PF00087; toxin_1.

DR ProDom; PD000206; Snake toxin_1.

DR PROSITE; PS00277; SNAKE_TOXIN; FALSE_NEG.

DR Blood coagulation; Cell adhesion; Toxin; 3D-structure.

KW 3D-structure.

FT DISULFID 3 22

FT DISULFID 3 22

FT DISULFID 17 37

FT DISULFID 39 51

FT DISULFID 52 57

FT SITE 43 45

FT STRAND 2 4

FT STRAND 14 16

FT STRAND 22 24

FT TURN 28 31

FT STRAND 36 37

FT STRAND 50 52

FT MW 6754 6754

SEQUENCE 59 AA; 20DDDC6A5D9DF9E41 CRC64;

CELL ATTACHMENT SITE (POTENTIAL).

CC

DR PIR; A42561; T65P5J.
 DR PDB; 1DPS; 20-DEC-94.

DR InterPro; IPR003571; Snake_toxin.

DR Pfam; PF00087; toxin_1.

DR ProDom; PD000206; Snake toxin_1.

DR PROSITE; PS00277; SNAKE_TOXIN; FALSE_NEG.

DR Blood coagulation; Cell adhesion; Toxin; 3D-structure.

KW 3D-structure.

FT DISULFID 3 22

FT DISULFID 17 37

FT DISULFID 39 51

FT SITE 43 45

FT STRAND 2 4

FT STRAND 14 16

FT STRAND 22 24

FT TURN 28 31

FT STRAND 36 37

FT STRAND 50 52

FT MW 6754 6754

SEQUENCE 59 AA; 20DDDC6A5D9DF9E41 CRC64;

CELL ATTACHMENT SITE (POTENTIAL).

CC

QY 23 RFCQNSSM-----TPHRHQSTPNYPNGLTMNYCRNPD 57
 SEQUENCE 52 AA; 5951 MW; C1E4006D43E05TA1 CRC64;

QY 24 RECLAPSSQHQSYYDIYIPTPTPHHTHTPTPHPHPTHTHHNPN 48
 SEQUENCE 13; Conservative 5; Mismatches 17; Indels 10; Gaps 1;

QY Best Local Similarity 28.9%; Pred. No. 1.4e+02;

Db DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Mambin (Glycoprotein IIb-IIIa antagonist) (Platelet aggregation inhibitor) (Dendroaspin).

OS Dendroaspis jamesoni; Kambosae (Eastern Jameson's mamba).

OC Eubariyota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Elapinae; Dendroaspis.

OX NCBI_TAXID=8619;

RN [1]

RP SEQUENCE.

RC TISSUE-Venom; MEDLINE=92273586; PubMed=1591238;

RA McDowell R.S.; Dennis M.S.; Louie A.; Shuster M.; Mulkerin M.G.,

RA Lacouras R.A.; Jaseja M.; Hyde E.T.; Lu X.; Williams J.A.;

RT "Mambin," a potent glycoprotein IIb-IIIa antagonist and platelet aggregation inhibitor structurally related to the short neurotoxins.;"

RT neurotoxins.;"

RL Biocchemistry 31:4766-4772(1992).

RN [2]

RP STRUCTURE BY NMR.

RX MEDLINE=9512853; PubMed=7634091;

RA Jaseja M.; Lu X.; Williams J.A.; Sutcliffe M.J.; Kakkar V.Y.,

RA Parslow R.A.; Hyde E.T.; Jaseja M.; Hyde E.T.; Lu X.; Williams J.A.;

RT "Three-dimensional structure of dendroaspin, an RGD-containing glycoprotein IIb-IIIa (alpha IIb-beta 3) antagonist with a neuritin fold.";

RT "The structure of dendroaspin, an RGD-containing glycoprotein IIb-IIIa (alpha IIb-beta 3) antagonist with a neuritin fold.";

RL J. Biochem. 226:861-868(1994).

CC -1- FUNCTION: INHIBITS ADP-INDUCED PLATELET AGGREGATION AND INHIBITS THE BINDING OF PURIFIED PLATELET FIBRINogen RECEPTOR GPIIb-IIIa

CC THE INHIBITION IS MOLECULARLY SELECTIVE.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE/SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the snake toxin family.

RESULT 14

NXSL-ASTST

STANDARD

PRT

60 AA.

ID NXSL

ASTST

PRT;

60 AA.

ID AC

P10461; P19005;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Short neurotoxin 1 ("Toxin A").

OS Astrotia stokesii (Stokes' sea snake).

OS Hydrophophis ornatus (Reef sea snake), and

OS Acalyptophis peronii (Sea snake).

OC Bukaoyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Hydrophiinae; Astrotoia.

NCBI_TAXID=8680, 8685, 8676;

RN [1]

RP SEQUENCE.

RC SPECIES=A_stokesi; TISSUE=Venom;

RX MEDLINE=79123997; PubMed=743209;

RA Maeda N.; Tamaiya N.;

RT "Three neurotoxins from the venom of a sea snake Astrotoia stokesii, including two long-chain neurotoxic proteins with amidated C-terminal."

RT Biochem. J. 213:31-38(1983).

RN [2]

RP COMPOSITION OF TRYPTIC PEPTIDES.

RC SPECIES=H_ornatus; TISSUE=Venom;

RX MEDLINE=33308533; PubMed=61615431;

RA Tamaiya N.; Maeda N.; Coquer H.G.;

RA "Neurotoxins from the venoms of the sea snakes Hydrophophis ornatus and Acalyptophis peronii."

RT Biochem. J. 213:31-38(1983).

RN [3]

RP SEQUENCE (MAJOR VARIANT).

RC SPECIES=A_peronii; TISSUE=Venom;

RX MEDLINE=88132805; PubMed=3471735;

RA Mori N.; Tu A.T.;

RT "Isolation and primary structure of the major toxin from sea snake Acalyptophis peronii, venom."

RT

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:30:34 ; Search time 94 Seconds
 (without alignments)
 244.326 Million call updates/sec

Title: US-10-088-548-6
 Perfect score: 523
 Sequence: 1 VRQCYHGNGQSYRGTFSTIV. STRWEYCNLTRCSDTEGTVV 89

Scoring table: BLOSUM62
 Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 113503

Minimum DB seq length: 0

Maximum DB seq length: 89

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mnh:*
8: sp_orcanelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodont:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
```

17	51.5	9.8	72	12	Q91ND7 cactus virus
18	51.5	9.8	87	12	Q8BBA5 human respi
19	51.5	9.8	87	12	Q8BBA4 human respi
20	51	9.8	66	15	Q9QJ4 human immun
21	51	9.8	83	12	Q8V5h6 human respi
22	51	9.8	88	15	Q9DXN2 human immun
23	50.5	9.7	57	10	Q8HS3 oryza sativ
24	50.5	9.7	80	12	Q8V5i6 human respi
25	50.5	9.7	83	12	Q8BBA3 human respi
26	50.5	9.7	87	12	Q8V5i7 human respi
27	50	9.6	73	15	Q72408 human immun
28	50	9.6	83	12	Q91b86 human respi
29	50	9.6	83	12	Q8V5i2 human respi
30	50	9.6	83	12	Q8BBA8 human respi
31	50	9.6	94	15	Q9ig35 human immun
32	50	9.6	88	15	Q9Dk9 white spot
33	49.5	9.5	65	2	Q8TOX4 mesobuthus
34	49.5	9.5	65	2	Q9EZG6 streptocooc
35	49.5	9.5	69	2	Q9z3a6 unidentifie
36	49.5	9.5	71	15	Q76655 human immun
37	49.5	9.5	72	5	Q8Mq9 schistosoma
38	49.5	9.5	76	12	Q8vad4
39	49.5	9.5	77	10	Q39403 brassica ca
40	49.5	9.5	79	5	Q44062 apicomplexa
41	49.5	9.5	80	12	Q91udi human respi
42	49.5	9.5	83	12	Q9TUD1
43	49.5	9.5	83	12	Q8V5h5 human respi
44	49.5	9.5	87	12	Q8V5i4 human respi
45	49.5	9.5	87	15	Q90468 human immun

ALIGNMENTS

RESULT 1					
ID	Q9UMI2	PRELIMINARY;	PRT;	53	AA.
AC	Q9UMI2;				
DT	01-MAY-2000 (TREMBLrel_13, Created)				
DT	01-MAY-2000 (TREMBLrel_13, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel_23, Last annotation update)				
DE	PLG protein (Fragment).				
GN	PLG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo-				
OX	NCBI_TAXID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85023311; PubMed=6148961;				
RA	Malinovski D.P., Sadler J.B., Davie E.W.;				
RT	"Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen"; Biochemistry 23:4243-4250(1984);				
RL	-1 - SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.				
CC	DR EMBL: K02921; AAA0123.1; -				
DR	HSSP; P00747; 2PK4.				
DR	IPI00001; Kringle.				
PFAM	PF00051; Kringle_1.				
PRINTS	PR00018; KRINGLE.				
PRODOM	PD000395; Kringle_1.				
SMART	SM00130; KS: 1				
PROSITE	PS00021; KRINGLE_1; FALSE_NEG.				
DR	PS50070; KRINGLE_2; 1.				
KW	Glycoprotein; Kringle.				
FT	NON_TER				
SQ	SEQUENCE 53 AA; 5893 MW;				
Query Match	42.6%	Score 223;	DB 4;	Length 53;	
Best Local Similarity	82.3%	Pred. No. 1.e-18;			
Matches	37;	Conservative 4;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1 VRQCYHGNGQSYRGTFSTIVGTCQSMTPHRHORTOPENYPN 45				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query ID	Match ID	Length	DB	Description
1	223	42.6	53	4	Ogumi2 homo sapien
2	190	36.3	60	4	Ogumki7 homo sapien
3	141	27.0	25	4	Ogud88 homo sapien
4	127.5	24.4	75	6	Q9BGN9 bos taurus
5	59.5	11.4	86	15	Q90rv4 human immun
6	56	10.7	87	15	Q90bu2 human immun
7	55.5	10.6	87	10	Q8H44 oryza sativ
8	53.5	10.2	85	16	Q8nts2 corynebacte
9	52.5	10.0	82	15	Q9YL18 human immun
10	52.5	10.0	87	12	Q8V5i3 human respi
11	52.5	10.0	88	15	Q9id04 human immun
12	52.5	10.0	89	15	Q9id03 human immun
13	52	9.9	39	6	Q9MFZ7
14	52	9.9	46	13	Q9Pw8 gallus galli
15	52	9.9	67	15	Q9jJh2 human immun
16	52	9.9	76	16	Q9837 streptomyce

			SQ	SEQUENCE	25 AA;	2928 MW;	BEEDDA4C62FA480A8 CRC64;
Db	8 VDCHGDCQSRTGTSSTTGKQCQSSMTPHRIOKTENYN 52						
RESULT 2			Query Match	Score 27.08;	DB 4;	Length 25;	
Q9DKJ7	PRELIMINARY;	PRT;	Best Local Similarity	96.0%;	Pred. No. 1.e-09;		
ID Q9DKJ7			Matches 24;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
AC OC							
DT 01-MAY-2000 (TREMBLrel. 13; Created)							
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)							
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)							
DE Apolipoprotein(a) (Fragment).							
GN APOA.							
OS Homo sapiens (Human).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX NCBI_TaxID=9606;							
RN [1]							
RP SEQUENCE FROM N.A.							
RX MEDLINE=2118105; PubMed=11285247;							
RA Osofrikova M.; Kraft, H.-G.; Ehnholt C.; Uttermann G.;							
RT "Single nucleotide polymorphisms in exons of the apo(a) Kringle IV							
RT types 6 to 10 domain affect up-regulation of plasma concentrations and have							
RT different patterns in Africans and Caucasians.";							
RL Hum. Mol. Genet. 10: 815-824 (2001).							
-1 SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.							
CC DR 60 AA; AF158657; AAFO3676..1. -.							
DR HSSP: P00747; IKRN.							
DR InterPro; IPR000001; Kringle.							
DR Pfam; PF00051; kringle_1.							
DR PRODom; PD00095; Kringle_1.							
DR SMART; SM00130; KR_1.							
DR PROSITE; PS00021; KRINGLE_1; 1.							
DR PROTEIN; PS50070; KRINGLE_2; 1.							
KW Glycoprotein; Kringle; Lipoprotein.							
FT NON_TER 1 1							
FT NON_TER 60 60							
SQ SEQUENCE 60 AA; 6739 MW; 5719AA26B3E0FF1D CRC64;							
Query Match	Score 36.38%;	DB 4;	Length 60;				
Best Local Similarity	69.88%;	Pred. No. 8.e-15;					
Matches 30;	Conservative 6;	Mismatches 7;	Indels 0;	Gaps 0;			
QY 47 GLTMNCRNPDAADTGPNCTTDPSIRWEYCNLTRCSPEGYV 89							
Db 1 GDTRICRNPDAEIRPWCYTMDPSYRWEYCNLQCLVTESSLV 43							
Query Match	Score 190;	DB 4;	Length 60;				
Best Local Similarity	69.88%;	Pred. No. 8.e-15;					
Matches 30;	Conservative 6;	Mismatches 7;	Indels 0;	Gaps 0;			
QY 47 GLTMNCRNPDAADTGPNCTTDPSIRWEYCNLTRCSPEGYV 89							
Db 1 GDTRICRNPDAEIRPWCYTMDPSYRWEYCNLQCLVTESSLV 43							
Query Match	Score 39.38%;	DB 4;	Length 60;				
Best Local Similarity	69.88%;	Pred. No. 8.e-15;					
Matches 30;	Conservative 6;	Mismatches 7;	Indels 0;	Gaps 0;			
QY 47 GLTMNCRNPDAADTGPNCTTDPSIRWEYCNLTRCSPEGYV 89							
Db 1 GDTRICRNPDAEIRPWCYTMDPSYRWEYCNLQCLVTESSLV 43							
RESULT 3							
Q9UD88	PRELIMINARY;	PRT;	25 AA.				
ID Q9UD88							
AC Q9UD88;							
DT 01-MAY-2000 (TREMBLrel. 13; Created)							
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)							
DT 01-OCT-2002 (TREMBLrel. 22; Last annotation update)							
DE apo(a) KRINGLE 4-3'; apo(A) KRINGLE type 5 (Fragment).							
OS Homo sapiens (Human).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX NCBI_TaxID=9606;							
RN [1]							
RP SEQUENCE FROM N.A.							
RX MEDLINE=94060120; PubMed=7848387;							
RA Pfaffinger D., Mc Lean J., Scam A. M.;							
RT "Amplification of human apo(a) Kringle 4-3' from blood lymphocyte							
RT DNA."							
RL Bichochim. Biophys. Acta 1225:107-109(1993).							
DR HSSP; P00747; IKRN.							
DR InterPro; IPR000001; Kringle.							
KW Glycoprotein; Kringle_1.							
FT NON_TER 1 1							
FT NON_TER 25 25							
SQ SEQUENCE 25 AA; 2928 MW; 829EEEFC49701B1 CRC64;							
Query Match	Score 24.4%;	DB 6;	Length 75;				
Best Local Similarity	52.8%;	Pred. No. 2.1e-07;					
Matches 19;	Conservative 9;	Mismatches 7;	Indels 1;	Gaps 1;			
QY 51 NYCRNPDADT-GPNCFTDPSTRWEYCNLRCSETE 85							
Db 1 NYCRNPDAEIRPWCYTMDPSYRWEYCNLQCLVTESSLV 36							
Query Match	Score 24.4%;	DB 6;	Length 75;				
Best Local Similarity	52.8%;	Pred. No. 2.1e-07;					
Matches 19;	Conservative 9;	Mismatches 7;	Indels 1;	Gaps 1;			
QY 51 NYCRNPDADT-GPNCFTDPSTRWEYCNLRCSETE 85							
Db 1 NYCRNPDAEIRPWCYTMDPSYRWEYCNLQCLVTESSLV 36							
RESULT 5							
Q9ORV4	PRELIMINARY;	PRT;	86 AA.				
ID Q9ORV4							
AC Q9ORV4;							
DT 01-DEC-2001 (TREMBLrel. 19; Created)							
DT 01-DEC-2001 (TREMBLrel. 19; Last sequence update)							
DT 01-OCT-2002 (TREMBLrel. 22; Last annotation update)							
DE Envelope glycoprotein (Fragment).							
ENV.							
OS Human immunodeficiency virus 1.							
OC Viruses; Retroviridae; Lentivirus.							
OX NCBI_TaxID=11676;							
RN [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=D_331V;							
RC Machado D.M., Delwart E.L., Diaz R.S., Oliveira C.F., Rawal B.D.,							
RA							

RA	Sullivan M., Gwinn M., Clark K.A., Busch M.P.; RT "Use of the Dual Sensitive/Less-Sensitive (Detuned) EIA Strategy for Targeting Genetic Analysis of HIV-1 to Recently Infected U.S. Blood Donors." ;
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120; 1.
KW	AIDS; Coat protein; Glycoprotein.
FT	NON_TER 1
FT	NON_TER 1
SEQUENCE	86 AA; 9895 MW; 1A0C197C8C58A808 CRC64;
QY	Query Match 41 ENYPNDGLTM-----NYCRNPDAADT-----GPWCFTTD-PSIRWEYCN-LT 79 Best Local Similarity 30.0%; Pred. No. 20; Gaps 4; Matches 21; Conservative 10; Mismatches 18; Indels 21; Length 86;
Db	10 ENFTDNRKTIIQNQSYGIVCYCRPNNTTRKIHIGGXVFTTDLIGDIRKAYCNISLT 69
QY	80 RCSDDTESTVV 89
Db	70 KWDTLQKIV 79
RESULT 6	Q9OBH2 ID Q9OBH2 PRELIMINARY; PRT; 87 AA.
AC	Q9OBH2; AC
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-OCT-2002 (TREMBLrel. 19, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	Envelope glycoprotein (fragment).
GN	EN.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11676;
RN	RP SEQUENCE FROM N.A.
RC	STRAIN=P64-49;
RA	Collins K., Quinones-Mateu M., Wu M., Laze H., Johnson J., Hirsch C., Toossi Z., Arts E.;
RA	"TB-mediated Site Specific Increase in HIV-1 Quasispecies Diversity May Lead to the Observed Greater HIV-1 Heterogeneity in Patients Co-infected with Tuberculosis.", Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RT	DR; IPR000777; GP120.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120; 1.
KW	AIDS; Coat protein; Glycoprotein.
FT	NON_TER 1
FT	NON_TER 87
SEQUENCE	87 AA; 9930 MW; 1D246B516BDD1F2C CRC64;
QY	Query Match 45 NDGTMTYCRNPDAADT-----GP-----WCFTTD--PSIRWEYCNLTCSDIE 85 Best Local Similarity 32.7%; Pred. No. 51; Gaps 4; Matches 17; Conservative 9; Mismatches 14; Indels 12; Length 87;
Db	16 NESYQIN CTRPNNNTTRKSYHIGPQRFYANGDIKGIRKWAICNVSAAWNE 66
RESULT 7	Q8H444 ID Q8H444 PRELIMINARY; PRT; 87 AA.
AC	Q8H444;
DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 23, Last annotation update)
DE	Envelope glycoprotein (Fragment).
GN	P0407H12-22 protein.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentivirus.

OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metazoa; Cetartiodactyla; Ruminantia; Peccota; Bovoidea;
 OC Bovidae; Bovine; Bos.
 NCBI_TaxID=9913;

[1]
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20380839; PubMed=10920240;
 RA Sonstegard T.S., Garrett W.M., Ashwell M.S., Bennett G.L.,
 RA Kappes S.M., Van Tassell C.P.;
 RT Comparative map alignment of BTA27 and HSA4 and 8 to identify
 conserved segments of genome containing fat deposition QTL.";
 RL Mamm. Genome 11:682-688(2000).
 DR AF230195; AAF:9125.1; -.
 DR HSSP_P00730; ITPG.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; kringle_1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS0118; EGF_2; 1.
 DR Glycoprotein; Kringle.
 FT NON_TER 1 1
 FT NOLTER 39 39
 SQ SEQUENCE 39 AA; 4296 MW; BDE3A28B38A67ECB CRC64;

Query Match 9.9%; Score 52; DB 6; Length 39;
 Best Local Similarity 60.0%; Pred. No. 61;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYHNGGTYRGTST 18
 ||| :|||:|||:
 Db 23 CYKDQYAYRGTST 37

RESULT 14

Q9PWW8 PRELIMINARY; PRT; 46 AA.
 AC Q9PWW8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE Riboflavin binding protein precursor (fragment).
 GN Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Gallus.
 NCBI_TaxID=9031;

RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 RX MEDLINE=88298752; PubMed=3403516;
 RA Zheng D.B., Lin H.M., Peo J.J., White H.B.;
 RT "Chicken riboflavin-binding protein";
 RL J. Biol. Chem. 263:11126-11129(1988).
 DR AB02234; BAA7129; BAA7128; -.
 DR InterPro; IPR004269; Folate_rec.
 DR Pfam; PF03034; Folate_rec; 1.

KW SIGNAL. 1 17
 FT CONFLICT 31 31 N -> K (IN REF. 2).
 SQ SEQUENCE 46 AA; 5136 MW; 4E015B6A6DE7AERF CRC64;

Query Match 9.9%; Score 52; DB 13; Length 46;
 Best Local Similarity 28.2%; Prod. No. 73; Mismatches 5; Indels 4; Gaps 1;

OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metazoa; Cetartiodactyla; Ruminantia; Peccota; Bovoidea;
 OC Bovidae; Bovine; Bos.
 NCBI_TaxID=9913;

[1]

RN

RP

SEQUENCE FROM N.A.

RX

Sonstegard T.S., Garrett W.M., Ashwell M.S., Bennett G.L.,

RA Kappes S.M., Van Tassell C.P.;

RT Comparative map alignment of BTA27 and HSA4 and 8 to identify
conserved segments of genome containing fat deposition QTL.";

RL Mamm. Genome 11:682-688(2000).

DR AF230195; AAF:9125.1; -.

DR HSSP_P00730; ITPG.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR000001; Kringle.

DR Pfam; PF00051; kringle_1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS0118; EGF_2; 1.

DR Glycoprotein; Kringle.

FT NON_TER 1 1

FT NOLTER 39 39

SQ SEQUENCE 39 AA; 4296 MW; BDE3A28B38A67ECB CRC64;

Query Match 9.9%; Score 52; DB 6; Length 39;
 Best Local Similarity 60.0%; Pred. No. 61;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY

4 CYHNGGTYRGTST 18

||| :|||:|||:<

Db 23 CYKDQYAYRGTST 37

SEQUENCE 67 AA; 7564 MW; 7969874F7D8BB6E CRC64;

Query Match 9.9%; Score 52; DB 15; Length 67;

Best Local Similarity 32.7%; Pred. No. 1.1e+02;

Matches 16; Conservative 8; Mismatches 13; Indels 12; Gaps 3;

QY

53 CRNPDAIT-----GPWCFTTD-PSTIRWEYCMLTRC--SDIEGTYY 89

||| :|||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 14 CTRPDNNTRRGTHIGPKAFFATDIGNTRQAHCTNSRARNNTLGQIV 62

Search completed: September 29, 2003, 08:35:46

Job time : 97 secs

OS Mamillaria; Metazoa; Cetartiodactyla; Ruminantia; Peccota; Bovoidea;
 OC Bovidae; Bovine; Bos.
 NCBI_TaxID=9913;

[1]

RN

RP

SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Hamajima S.;

RN [2]

RN

RP

SEQUENCE FROM N.A.

RC TISSUE=liver;

RX MEDLINE=88298752; PubMed=3403516;

RA Zheng D.B., Lin H.M., Peo J.J., White H.B.;

RT "Chicken riboflavin-binding protein";

RL J. Biol. Chem. 263:11126-11129(1988).
 DR AB02234; BAA7129; BAA7128; -.

DR InterPro; IPR004269; Folate_rec.

DR Pfam; PF03034; Folate_rec; 1.

KW SIGNAL. 1 17

FT CONFLICT 31 31 N -> K (IN REF. 2).

SQ SEQUENCE 46 AA; 5136 MW; 4E015B6A6DE7AERF CRC64;

Query Match 9.9%; Score 52; DB 13; Length 46;

Best Local Similarity 28.2%; Prod. No. 73; Mismatches 5; Indels 4; Gaps 1;

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	86	22	AAV72947 Human apolipoprotein A1
2	413	81.3	85	21	AAB08413 Human apolipoprotein A1
3	405	79.7	79	18	AAN19256 Human apolipoprotein A1
4	274.5	54.0	79	17	AAN07546 Rhesus Kringle
5	258.5	50.9	79	17	AAN07548 Rhesus Kringle
6	258.5	50.9	82	21	AAV7719 Human plasminogen kringle
7	258.5	50.9	84	10	AAB93230 Human plasminogen kringle
8	258.5	50.9	84	11	AAB07545 Human plasminogen kringle
9	256.5	50.5	79	17	AAB07546 Human plasminogen kringle

% SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution and is derived by analysis of the total score distribution.

XX Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated
PT diseases, e.g. cancer and rheumatoid arthritis, has human
PT apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
PT sequence -
XX Claim 3: Page 47; 50pp; English.
XX The present sequence is human LK8 protein which contains the amino
CC acid sequence of human apolipoprotein(a) kringle domain V38
CC (V38). The human apolipoprotein(a) kringle domains IV36 (LK6
CC protein), IV37 (LK7 protein) and V38 (LK8 protein) together form the
CC angiogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are
CC inhibitors of endothelial cell proliferation, cell migration and
CC normal development of capillaries in the chick embryo chorioallantoic
CC membrane (CAM). LK68 protein, its single kringles or their functional
CC equivalents, are useful for treating angiogenesis-mediated diseases,
CC such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic
CC disease in animals or humans. LK68 is useful as an anticancer agent and
CC also for inhibiting primary tumour growth.

XX Sequence 86 AA;

Query Match Similarity 100.0%; Score 508; DB 22; Length 86;
Best Local Similarity 100.0%; Pred. No. 1e-422; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EODCMFGNGNGYRKAKATVTPCCEWAQEPHRHSTFIGTNWAGLEKKNYCRNPDD 60

1 EODCMFGNGNGYRKAKATVTPCCEWAQEPHRHSTFIGTNWAGLEKKNYCRNPDD 60

61 INGPWCYTMAPRKLFYCDIPLCASS 86

61 INGPWCYTMAPRKLFYCDIPLCASS 86

RESULT 3 AAW19256

ID AAW19256 standard; Peptide: 79 AA.

AC AAW19256;

XX XX AC AAW19256;

XX DT 27-FEB-1998 (first entry)

XX Human plasminogen Kringle 5 fragment.
DE DE Human plasminogen Kringle 5 fragment.

XX XX KW KW Plasminogen; Kringle 5; cell proliferation inhibitor; angiogenesis;

XX XX KW KW diagnosis; therapeutic.

XX OS OS Homo sapiens.

XX XX PN WO9723500-A1.

XX XX PD 03-JUL-1997.

XX PF 13-DEC-1996; 96WO-US20447.

XX PR 12-DEC-1996; 96US-073528.

XX PR 13-DEC-1995; 95US-0008519.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Cao Y, Folkman MJ;

XX DR WPI; 1997-350965/32.

XX This sequence is an isolated fragment of the Kringle 5 peptide
CC corresponding to amino acid 462 of the human plasminogen protein which
CC can be used in a novel method to inhibit endothelial cell proliferation
CC activity. The protein can be used to treat angiogenesis mediated
CC diseases, e.g. haemangioma, solid tumours, leukaemia, metastasis,
CC telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial
CC angiogenesis, plaque neovascularisation, coronary or cerebral

XX Disclosure; Fig 6; 163pp; English.
PS PS
XX CC The specification describes a human polypeptide which is a potent
CC angiogenesis inhibitor, and is designated KED. KED polypeptide, kringle
CC proteins, or a kringle derived from human tissue Plasminogen activator
CC (PA) protein are used to inhibit angiogenesis. Kringle protein, KED
CC or tPA are useful for treating tumours, as well as atherosclerosis,
CC arthritis, retinopathy and other similar diseases. KED is also useful
CC for the treatment of diseases such as bronchial vascular congestion,
CC inflammatory bowel disease, adult respiratory distress syndrome,
CC Castlemann's disease, psoriasis, hepatitis, renal disease
CC and haemangioma. The present sequence represents kringle 5 of human
CC plasminogen, which is used in the course of the invention.
XX Sequence 85 AA;
Query Match Similarity 81.3%; Score 413; DB 21; Length 85;
Best Local Similarity 80.0%; Pred. No. 2.3e-33; Indels 0; Gaps 0;
Matches 68; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
XX QY 1 EQDCMFGNGNGYRKAKATVTPCCEWAQEPHRHSTFIGTNWAGLEKKNYCRNPDD 60
Db 1 EODCMFGNGNGYRKAKATVTPCCEWAQEPHRHSTFIGTNWAGLEKKNYCRNPDD 60
XX QY 61 INGPWCYTMAPRKLFYCDIPLCASS 85
Db 61 VGGPWCYTNDRLKLYCDVPCCAA 85
RESULT 3 AAW19256
ID AAW19256 standard; Peptide: 79 AA.
AC AAW19256;
XX XX AC AAW19256;
XX DT 27-FEB-1998 (first entry)
XX Human plasminogen Kringle 5 fragment.
DE DE Human plasminogen Kringle 5 fragment.
XX XX KW KW Plasminogen; Kringle 5; cell proliferation inhibitor; angiogenesis;
XX XX KW KW diagnosis; therapeutic.

XX OS OS Homo sapiens.

XX XX PN WO9723500-A1.

XX XX PD 03-JUL-1997.

XX PF 13-DEC-1996; 96WO-US20447.

XX PR 12-DEC-1996; 96US-073528.

XX PR 13-DEC-1995; 95US-0008519.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Cao Y, Folkman MJ;

XX DR WPI; 1997-350965/32.

XX This sequence is an isolated fragment of the Kringle 5 peptide
CC corresponding to amino acid 462 of the human plasminogen protein which
CC can be used in a novel method to inhibit endothelial cell proliferation
CC activity. The protein can be used to treat angiogenesis mediated
CC diseases, e.g. haemangioma, solid tumours, leukaemia, metastasis,
CC telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial
CC angiogenesis, plaque neovascularisation, coronary or cerebral

CC collaterals; arteriovenous malformations; ischemic limb angiogenesis,
 CC corneal diseases; rubosis; neovascular glaucoma; diabetic retinopathy,
 CC retroocular fibroplasia; arthritis; diabetic neovascularisation;
 CC muscular degeneration; vesiculogenesis; haematozoensis; ovulation,
 CC fractures; keloids; angiogenesis; placenta; cat scratch fever; and to stimulate wound
 CC healing. The protein and antibodies generated from it can be used to
 CC screen for agonists and antagonists or in detection, imaging and
 CC diagnosis.

XX SQ Sequence 79 AA;
 XX SQ Sequence 79 AA;
 Query Match 79.7%; Score 405; DB 18; Length 79;
 Best Local Similarity 84.6%; Pred. No. 1.3e-32; Indels 0; Gaps 0;
 Matches 66; Conservative 5; Mismatches 7;

QY 4 CMFGNGKGYRGKKATTVTGTPCQEWAQEPHRHSTIPTGTNKWAGLEKNYCRNPDDING 63
 Db 1 CMFGNGKGYRGKRAVTVTGTPCQEWAQEPHRHSTIPTGTNKWAGLEKNYCRNPDDING 60

QY 64 PWCTTMAPRKFDYCDIP 81
 Db 61 PWCTTMAPRKFDYCDIP 78

RESULT 4
 AAW07546
 ID AAW07546 standard; protein; 79 AA.
 XX AC AAW07546;
 XX DT 21-JUN-1997 (first entry)
 XX DE Rhesus Kringle 1.
 XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 XX KW macular degeneration; diabetic retinopathy.
 XX OS Rhesus.
 XX PN WO9635774-A2.
 XX PR 14-NOV-1996.
 XX PF 26-APR-1996.
 XX PR 08-MAR-1996.
 XX PR 26-APR-1995.
 XX PR 22-FEB-1996.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Cao Y, Folkman MJ, Lin J, Oreilly MS, Sim KL;
 XX DR WPI; 1996-518662/51.

XX Use of angiostatin fragments or aggregates - for inhibiting
 PT endothelial cell proliferation and treating angiogenesis-mediated
 PT diseases, e.g. cancer, arthritis or diabetic retinopathy
 XX Claim 4; Pages 104-105; 203pp; English.

PT The invention relates to new methods and compositions for
 PT inhibiting endothelial cell proliferation, using as active component
 XX an angiostatin fragment, a combination of angiostatin fragments, or
 XX an angiostatin fragment. The fragment is preferably derived from murine,
 CC human, Rhesus, porcine or bovine Plasminogen and is a kringle 1,
 CC kringle 2, kringle 3, kringle 2-3, kringle 1-2, kringle 1-3, kringle 1-2, kringle
 CC 1-4 or kringle 1-ABKLs protein. The aggregate angiostatin has a Mol. Wt.
 CC of 45-65 kD and is derived from a plasminogen fragment beginning at
 CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
 CC bovine plasminogen. The active component can be used for treating
 CC angiogenesis-mediated diseases such as cancer, arthritis, macular
 CC degeneration and diabetic retinopathy. It can also be used to develop
 CC antibodies for use in diagnosis, detection and therapy.

CC The present sequence, bovine kringle 1, is a specific angiostatin
 CC fragment which can be used in the invention, and represents amino
 CC acids 6-84 of Rhesus angiostatin.
 XX Sequence 79 AA;

Query Match 54.0%; Score 274.5; DB 17; Length 79;
 Best Local Similarity 58.8%; Pred. No. 9.4e-20;
 Matches 47; Conservative 8; Mismatches 24; Indels 1; Gaps 1;

QY 4 CMFGNGKGYRGKKATTVTGTPCQEWAQEPHRHSTIPTGTNKWAGLEKNYCRNPDDING 63
 Db 1 CKWYNGKGYRGTMSTMSKTRGTTGTCRWSSPSR PPEPSRTHPSEGLENTCRNPDDING 59

QY 64 PWCTTMAPRKFDYCDIPLC 83
 Db 60 PWCTTMAPRKFDYCDIPC 79

RESULT 5
 AAW07548
 ID AAW07548 standard; protein; 79 AA.
 XX AC AAW07548;
 XX DT 21-JUN-1997 (first entry)
 XX DE Bovine kringle 1.
 XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
 XX KW macular degeneration; diabetic retinopathy.
 XX OS WO9635774-A2.
 XX PN WO9635774-A2.
 XX PD 14-NOV-1996.
 XX PF 26-APR-1996.
 XX PR 08-MAR-1996.
 XX PR 26-APR-1995.
 XX PR 22-FEB-1996.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Cao Y, Folkman MJ, Lin J, Oreilly MS, Sim KL;
 XX DR WPI; 1996-518662/51.

XX Use of angiostatin fragments or aggregates - for inhibiting
 PT endothelial cell proliferation and treating angiogenesis-mediated
 PT diseases, e.g. cancer, arthritis or diabetic retinopathy
 XX Claim 4; Page 106; 203pp; English.

PT The invention relates to new methods and compositions for
 PT inhibiting endothelial cell proliferation, using as active component
 XX an angiostatin fragment. The fragment is preferably derived from murine,
 XX an angiostatin fragment. The fragment is a kringle 1,
 CC human, Rhesus, porcine or bovine Plasminogen and is a kringle 1,
 CC kringle 2, kringle 3, kringle 2-3, kringle 1-2, kringle 1-3, kringle 1-2, kringle
 CC 1-4 or kringle 1-ABKLs protein. The aggregate angiostatin has a Mol. Wt.
 CC of 45-65 kD and is derived from a plasminogen fragment beginning at
 CC approximately amino acid number 98 of murine, human, Rhesus, porcine or
 CC bovine plasminogen. The active component can be used for treating
 CC angiogenesis-mediated diseases such as cancer, arthritis, macular
 CC degeneration and diabetic retinopathy. It can also be used to develop
 CC antibodies for use in diagnosis, detection and therapy.

CC The present sequence, bovine kringle 1, is a specific angiostatin
 CC fragment which can be used in the invention, and represents amino
 CC acids 6-84 of Rhesus angiostatin.
 XX Sequence 79 AA;

CC acids 6-84 of bovine angiotatin.
 XX Sequence 79 AA;
 SQ Query Match 50.9%; Score 258.5; DB 17; Length 79;
 Best Local Similarity 57.5%; Pred. No. 3.5e-18;
 Matches 46; Conservative 7; Mismatches 26; Indels 1; Gaps 1;
 SQ Sequence 82 AA;

QY 4 CMFGNGKGRGKKATITVGPQWAAEPHSRSTRIPGNKAGLENYCRNPDDING 63
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1 CKTGNGQUTRGTAETKSGTVCQWSATSPH-VPKFSPERPLAGLEENYCRNPDDING 59

QY 64 PWCTNPNPKRLFDYCDIPLC 83
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 PWCTNPDVKRYDIDCPEC 79

RESULT 6
 AAY77719
 ID AAY77719 standard; protein; 82 AA.
 XX AC AAY77719;
 XX DT 12-MAY-2000 (first entry)
 XX DE Human plasminogen kringle 1 sequence.
 XX KW Kringle 1; plasminogen; anti-angiogenic; angiogenesis; angiostatin;
 KW cytostatic; antiarthritic; antineuritic; antidiabetic; ophthalmological;
 KW immunosuppressant; vasotropin; vulnerable; vascularization;
 KW dermatological; cancer; tumour; birth control; vascularization.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 PH Region 36..73 /note= "specifically claimed fragment (AAY77722)"
 FT XX
 PN WO200003726-A1.
 XX PD 27-JAN-2000.
 XX PF 07-JUL-1999; 99WO-US15271.
 XX PR 14-JUL-1998; 98W5-0092831.
 XX DR (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA PI J1 R, Trail PA;
 XX PT WPI: 2000-171200/15.
 XX Novel lysine binding fragments angiotatin used as antiangiogenic
 PT agents in the treatment of cancer, diabetic retinopathy, rheumatoid
 PT arthritis, psoriasis, atherosclerotic plaque formation, and other
 PT antiangiogenesis diseases -
 XX Disclosure; Fig 2; 30pp; English.
 PS The invention provides fragments of kringle 1, 2 or 4 of human
 CC plasminogen that contain a lysine binding site and have anti-angiogenic
 CC activity. The peptides of the invention function as antiangiogenic
 CC agents, for the treatment process and diseases involving angiogenesis.
 CC Such diseases include cancers such as solid tumours, blood born tumours
 CC such as leukaemias, tumours metastasis, benign tumours such as
 CC hemangiomas, acoustic acuromas, neurofibromas, trichomas and pyogenic
 CC granulomas, rheumatoid arthritis, ocular angiogenic diseases such as
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC congenital graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Weber syndrome, myoclonic joints, angiobromia,
 CC neovascularization, telangiectasia, hemophilic joints, angiobromia,
 CC and wound granulation. The fragments are also useful in treatment of
 CC disease of excessive or abnormal stimulation of endothelial cells. These

CC diseases include intestinal adhesions, atherosclerosis, scleroderma, and
 CC hypertrrophic scars. The fragments can be used as birth control agents by
 CC preventing vascularization required for embryo transplantation. The
 CC present sequence represents the kringle 1 sequence of human plasminogen
 (angiotatin).
 SQ Sequence 82 AA;

Query Match 50.9%; Score 258.5; DB 21; Length 82;
 Best Local Similarity 54.3%; Pred. No. 3.7e-18;
 Matches 44; Conservative 9; Mismatches 27; Indels 1; Gaps 1;
 CC

QY 3 DCMEGNGKGRGKKATITVGPQWAAEPHSRSTRIPGNKAGLENYCRNPDDIN 62
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 2 ECKTGNGKUTRGTAETKSGTVCQWSATSPH-VPKFSPERPLAGLEENYCRNPDDPQ 60

QY 63 GPWCYTMMNPDKLFDYCDIPLC 83
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 61 GPWCYTMMDPKLFYCDIPLC 81

RESULT 7
 AAP93230 standard; peptide; 84 AA.
 ID AAP93230
 XX AC AAP93230;
 XX AC AAP93230;
 XX DT 25-MAR-2003 (updated)
 DT 03-APR-1990 (first entry)
 XX DE Plasminogen kringle 1 domain (residues 79-162).
 XX KW Plasminogen; activator; t-PA; fibrin; kringle domain;
 KW scu-PA;
 XX OS Homo sapiens.
 XX PN WO8910401-A.
 XX PD 02-NOV-1989.
 XX PP 23-MAR-1989; 89WO-US01255.
 XX PR 22-APR-1988; 88US-0184823.
 XX PA (COLB) COLLABORATIVE RES INC.
 XX PI Mao JI, Abercrombie DM;
 XX DR WPI: 1989-339965/46.
 XX DR N-FSDB; AAP92237.
 XX PT Modified plasminogen activator - having greater fibrin
 PT selectivity and circulating half-life.
 XX Disclosure; fig 3A; 80pp; English.
 XX Sequence 84 AA;

Query Match 50.9%; Score 258.5; DB 10; Length 84;
 Best Local Similarity 54.3%; Pred. No. 3.8e-18;
 Matches 44; Conservative 9; Mismatches 27; Indels 1; Gaps 1;
 CC

QY 3 DOMFGNGKGRGKKATITVGPQWAAEPHSRSTRIPGNKAGLENYCRNPDDIN 62
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 5 ECKTGNGKUTRGTAETKSGTVCQWSATSPH-VPKFSPERPLAGLEENYCRNPDDPQ 63

Qy	64 PWCYTMNPRKLEFDYCDIPLC 83 : . :	AC AAB08410; XX XX 20-DEC-2000 (first entry)
Db	60 PWCTTDPEKRYCDIPLC 79	DE Amino acid sequence of kringle 1 of human plasminogen.
RESULT 10		XX Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA; tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distress syndrome; Castelman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangioma.
ID AAP90598	standard; protein; 81 AA.	XX
AC AAP90598;		XX
XX		OS Homo sapiens.
DT 25-MAR-2003 (updated)		XX
DT 31-OCT-2002 (updated)		PN WO20049871-A1.
XX		XX
DE Synthetic N-terminal protein of truncated human tissue plasminogen activator (t-PA).		PD 31-AUG-2000.
XX		XX
KW t-PA; tissue plasminogen activator; thrombolytic; fibrinolytic; fibrin; ds;		PP 24-FEB-2000; 2000WO-US04798.
DE activator (t-PA).		XX
XX		PR 24-FEB-1999; 99US-0121341.
KW fibrinolytic; fibrin; ds;		PR 25-FEB-1999; 99US-0121633.
DE		PR 18-NOV-1999; 99US-0166176.
XX		XX
Synthetic.		PA (FORD-) FORD HEALTH SYSTEM HENRY.
XX		PA
PN WO8900191-A.		PI Dou D, Chopp M, Wang L, Mikkelsen T;
XX		XX
PD 12-JUN-1989.		DR WPI; 2000-572016/53.
XX		XX
PF 06-JUL-1988;	88WO-US02263.	PT Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
XX		PT
PR 06-JUL-1987;	87US-0070012.	CC
PR 20-APR-1988;	88US-0184121.	CC
XX		CC
(GEMY) GENETICS INST INC.		CC
XX		CC
PI Larsen GR, Ahern T, Langersafe P;		CC
XX		The specification describes a human polypeptide which is a potent angiogenesis inhibitor, and is designated KED. KED polypeptide, kringle proteins, or a kringle derived from human tissue plasminogen activator (t-PA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumors, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome, Castelman's disease, psoriasis, hepatitis, aneurysm, renal disease and haemangioma. The present sequence represents kringle 1 of human plasminogen, which is used in the course of the invention.
DR 1989-039648/05.		CC
DR N PSDB; AAN91194.		CC
XX		CC
PR Tissue plasminogen activator variants - having N-terminal domain replaced with first kringle region		CC
PT domain of plasminogen.		CC
XX		CC
PA Claim 1; Page 32; 36PP; English.		CC
XX		CC
CC Inserted in front of an N-terminal 1-82 AA truncated t-PA protein, new product has an increased affinity to fibrin, decreased reactivity with inhibitors and increased thrombolytic activity.		CC
CC (Updated on 31-OCT-2002 to add missing OS field.)		CC
CC (Updated on 25-MAR-2003 to correct PA field.)		CC
CC (Updated on 25-MAR-2003 to correct DR field.)		CC
XX		CC
SQ Sequence 81 AA:		CC
Query Match Score 254; DB 10; Length 81;		CC
Best Local Similarity 53.1%; Pred. No. 1e-17;		CC
Matches 43; Conservative 9; Mismatches 27; Indels 2; Gaps 1;		CC
Qy 3 DCMFONGKGYRKAKATVTGTPCQEWAAQEPHRHSTIPSTINKAGLEKKNYCRNPDDIN 62		CC
Db 2 ECKTNGKNYRGTMSTKNGATCQKWSSSTSP--HPRSPATHPSQEGLEENYCRNPNDPQ 59		CC
RESULT 12		CC
Qy 63 GPWCYTMNPRKLEFDYCDIPLC 83		Qy 63 GPWCYTMNPRKLEFDYCDIPLC 83
Db 60 GPWCYTDPEKRYCDIPLC 80		Db 62 GPWCYTDPEKRYCDIPLC 82
RESULT 11		XX
AAB08410	standard; Protein; 84 AA.	XX
ID AAB08410		XX
XX		XX

DE	K1 domain of plasminogen.	XX	XX	PR	25-NOV-1987;	87US-0125629.
KW	tissue plasminogen activator; analogue; K1 domain.	XX	XX	PR	28-JUN-1992;	94US-0827587.
XX	Homo sapiens.	XX	XX	PR	06-JUN-1994;	94US-0254485.
OS				XX		
XX	EP293934-A.	XX	XX	PA		(ZYMO) ZYMOGENETICS INC.
PN				PI		Foster DC;
XX				PI		
PD	07-DIC-1988.	XX	XX	WPI	1996-187699/19.	
XX	03-JUN-1988;	XX	XX	DR	N-PSDB; AAT27586.	
PF	88EP-0108949.	XX	XX			
XX	04-JUN-1987;	XX	XX	PT	Hybrid plasminogen activator comprises human tPA activator and N-terminal crosslinking domain from alpha2-plasmin inhibitor -	
PR	87US-0058217.	XX	XX	PT	N-terminal crosslinking domain from alpha2-plasmin inhibitor - useful to treat thrombosis and image blood clots	
XX				XX		
PA	(ZYMO) ZYMOGENETICS INC.	XX	XX	Example 3; Fig 4; 35PP; English.		
PA	(NOVO) NOVO IND AS.	XX	XX	PS		
PA	(EISA) EISA CO LTD.	XX	XX	CC	The Kringle K1 domain (AAR96221) of Plasminogen was incorporated into tissue plasminogen activator (tPA) (see also AAR96220) as a replacement for the native tPA Kringle 1 sequence, producing a novel plasminogen activator (see also AAR96222). This was performed by insertion of plasminogen K1 DNA (AAT27386) into a native tPA sequence (AAT27385), and expression in Escherichia coli RRI transformants (FERM P-92/2). Such protocols can be used to produce novel plasminogen activators that show increased clot lysing specificity or plasma half-lives.	
PA				CC	CC	
PA				CC	CC	
PI	Mulvihill ER, Nexo BA, Yoshitake S, Ikeda Y, Suzuki S;	XX	XX	CC	CC	
PI	Hashimoto A, Yuzuriha T;	XX	XX	CC	CC	
XX	WPI; 1988-347625/49.	XX	XX	CC	CC	
DR	N-PSDB; AAN81087.	XX	XX	CC	CC	
XX	New tissue plasminogen activator analogues with non-native K1-domain -	XX	XX	CC	CC	
PT	having higher fibrin specificity, and new encoding DNA sequences.	XX	XX	CC	CC	
PT	PS Disclosure; Page ?; ?PP; English.	XX	XX	CC	CC	
PS				CC	CC	
XX	Sequence 79 AA;	XX	XX	CC	CC	
CC	The K1 domain of plasminogen may be used to replace the K1 domain of t-PA to produce an analogue with greater specificity for fibrin than native t-PA.	XX	XX	CC	CC	
CC	(updated on 31-OCT-2002 to add missing OS field.)	XX	XX	CC	CC	
CC	(updated on 25-MAR-2003 to correct PA field.)	XX	XX	CC	CC	
CC	(updated on 25-MAR-2003 to correct PI field.)	XX	XX	CC	CC	
SQ	Sequence 79 AA;	XX	XX	CC	CC	
Query Match	49.5%	XX	XX	CC	CC	
Best Local Similarity	53.8%	XX	XX	CC	CC	
Matches	43; Conservative 9; Mismatches 27; Indels 1; Gaps 1;	XX	XX	CC	CC	
XX				CC	CC	
QY	4 CMFGNGKGYRKAKATTGTPCQENAAQEPHRHSTFTPGTNKWAGLEKNYCRNPDGDING 63	XX	XX	CC	CC	
Db	1 CKTGDKVGRGMSKTKNGITCQKWSSTSPhR-PFSPATHPSGELEYCRNPDNDPQG 59	XX	XX	CC	CC	
				CC	CC	
RESULT 14				CC	CC	
AAR94401				CC	CC	
ID	AAP94401 standard; protein; 78 AA.	XX	XX	CC	CC	
XX				CC	CC	
AC	AAP94401;	XX	XX	CC	CC	
XX				CC	CC	
DT	01-JUL-2002 (updated)	XX	XX	CC	CC	
DT	18-JUN-1990 (first entry)	XX	XX	CC	CC	
XX				CC	CC	
DE	Sequence encoding K1 domain of plasminogen.	XX	XX	CC	CC	
XX				CC	CC	
KW	Tissue plasminogen activator; tPA; alpha2-plasmin inhibitor; fibrinolytic; fibrin; thrombolytic; fibrin; thrombosis; blood clotting; protein engineering; kringle domain K1.	XX	XX	CC	CC	
XX				CC	CC	
OS	Synthetic.	XX	XX	CC	CC	
XX				CC	CC	
PN	US5504001-A.	XX	XX	CC	CC	
XX				CC	CC	
PD	02-APR-1996.	XX	XX	CC	CC	
XX				CC	CC	
PF	94US-0254485.	XX	XX	CC	CC	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:45:34 ; Search time 29 Seconds

(without alignment)
125.474 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508

Sequence: 1 EODCMFGNGKGYRGKKATTY. YTMNPKLKEDYCDIPLCASS 86

Scoring table: BiologM2

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:

222816

Minimum DB seq length: 0

Maximum DB seq length: 86

Post-processing: Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
 1: /cgn2_6/pctodata/1/iaa/5A_COMB_pep: *
 2: /cgn2_6/pctodata/1/iaa/5B_COMB_pep: *
 3: /cgn2_6/pctodata/1/iaa/6A_COMB_pep: *
 4: /cgn2_6/pctodata/1/iaa/6B_COMB_Pep: *
 5: /cgn2_6/pctodata/1/iaa/BCTUS_COMB_pep: *
 6: /cgn2_6/pctodata/1/iaa/backfillsl_pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	412	81.1	80	2 US-08-763-528A-6	Sequence 6, Appli
2	405	79.7	79	2 US-08-763-528A-6	Sequence 1, Appli
3	274.5	54.0	79	3 US-08-612-788-9	Sequence 9, Appli
4	274.5	54.0	79	3 US-09-066-028-9	Sequence 9, Appli
5	274.5	54.0	79	4 US-09-335-325-9	Sequence 9, Appli
6	258.5	50.9	79	7 US-08-612-788-11	Sequence 11, Appli
7	258.5	50.9	79	3 US-09-066-028-11	Sequence 11, Appli
8	258.5	50.9	79	4 US-09-335-325-11	Sequence 11, Appli
9	258.5	50.9	82	4 US-09-348-953-1	Sequence 1, Appli
10	256.5	50.5	79	2 US-08-612-788-8	Sequence 8, Appli
11	256.5	50.5	79	2 US-08-763-528A-2	Sequence 2, Appli
12	256.5	50.5	79	3 US-09-066-028-8	Sequence 8, Appli
13	256.5	50.5	79	4 US-09-335-325-8	Sequence 8, Appli
14	246.5	48.5	79	2 US-08-612-788-10	Sequence 10, Appli
15	246.5	48.5	79	3 US-09-066-028-10	Sequence 10, Appli
16	246.5	48.5	79	4 US-09-335-325-10	Sequence 10, Appli
17	241.5	47.5	79	2 US-08-612-788-7	Sequence 7, Appli
18	241.5	47.5	79	3 US-09-066-028-7	Sequence 7, Appli
19	241.5	47.5	79	4 US-09-335-325-7	Sequence 7, Appli
20	240	47.2	78	2 US-08-612-788-22	Sequence 22, Appli
21	240	47.2	78	3 US-09-066-028-22	Sequence 22, Appli
22	240	47.2	78	4 US-09-335-325-22	Sequence 22, Appli
23	235	46.3	94	4 US-09-348-953-2	Sequence 2, Appli
24	222	43.7	78	2 US-08-612-788-17	Sequence 17, Appli
25	222	43.7	78	2 US-08-613-528A-5	Sequence 5, Appli
26	222	43.7	78	2 US-09-066-028-17	Sequence 17, Appli
27	222	43.7	78	3 US-09-066-028-17	Query Match

ALIGNMENTS

RESULT 1
US-08-763-528A-6

; Sequence 6, Application US/08763528A

; Patent No. 5854221

; GENERAL INFORMATION:

; APPLICANT: Cao, Yihai

; TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jones & Askew, LLP

; STREET: 191 Peachtree Street, 37th Floor

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: US

; ZIP: 30303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/763,528A

; FILING DATE: 12-DEC-1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren, William L.

; REGISTRATION NUMBER: 36,714

; REFERENCE/DOCKET NUMBER: 05940-0251

; TELECOMMUNICATION INFORMATION:

; TELEFAX: 404-818-3700

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..80

; OTHER INFORMATION: /note= "kringle 5 - Figure 3"

; US-08-763-528A-6

; Query Match

; Score 11%; Score 412%; DB 2; Length 80;

Best Local Similarity 83.8%; Pred. No. 9.3e-40; Matches 67; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 CMFGNGKGYRKAKATVGTGTCQEWAAQEPHRHSTFPGTNKWAGLEKNYCRNPDGDING 63
 Db 1 CMFGNGKGYRKAKATVGTGTCQDWAAQEPHRHSTFPGTNKWAGLEKNYCRNPDGDGG 60

QY 64 PWCYTMNPKLFDYCDPLC 83
 Db 61 PWCYTMNPKLFDYCDVQC 80

RESULT 2 US-08-73-528A-1

; Sequence 1, Application US/08763528A
 ; PATENT NO. 5844211
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Folkman, M. Judah
 ; TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
 ; NUMBER OF SEQUENCES: 6
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 12-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/763,528A
 ; FILING DATE: 12-DEC-1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05940-0251
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-3799
 ; INQUIRIES FOR SEQ ID NO.: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 79 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rhesus monkey
 ; IMMEDIATE SOURCE:
 ; CLONE: K1
 ; US-08-612-788-9

Query Match 54.0% Score 274.5; DB 2; Length 79;
 Best Local Similarity 81.6%; Pred. No. 5.7e-39; Matches 66; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 CMFGNGKGYRKAKATVGTGTCQEWAAQEPHRHSTFPGTNKWAGLEKNYCRNPDGDING 63
 Db 1 CMFGNGKGYRKAKATVGTGTCQDWAAQEPHRHSTFPGTNKWAGLEKNYCRNPDGDGG 60

QY 64 PWCYTMNPKLFDYCDIP 81
 Db 61 PWCYTMNPKLFDYCDVP 78

RESULT 3 US-08-612-788-9
 ; Sequence 9, Application US/08612788

; Patent No. 5837682
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: U.S.
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-3799
 ; INQUIRIES FOR SEQ ID NO.: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 79 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rhesus monkey
 ; IMMEDIATE SOURCE:
 ; CLONE: K1
 ; US-08-612-788-9

Query Match 54.0% Score 274.5; DB 2; Length 79;
 Best Local Similarity 58.8%; Pred. No. 3.9e-44; Matches 47; Conservative 24; Indels 1; Gaps 1;

QY 4 CMFGNGKGYRKAKATVGTGTCQEWAAQEPHRHSTFPGTNKWAGLEKNYCRNPDGDING 63
 Db 1 CKTGNGNYRTGMSKTRGTTCKWSSTSHER-PFESRATHPSEGLENNTCRNPDNSOG 59

QY 64 PWCYTMNPKLFDYCDPLC 83
 Db 60 PWCYTMNPKLFDYCDIP 79

RESULT 4 US-09-066-028-9
 ; Sequence 9, Application US/09066028
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 FILING DATE: US/09/066,028
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 PRIORITY APPLICATION NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 79 amino acids
 FRAGMENT TYPE: N-terminal
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 LENGTH: 79 amino acids
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rhesus monkey
 IMMEDIATE SOURCE:
 CLONE: K1
 US-09-066-028-9

Query Match 54.0%; Score 274.5%; DB 3; Length 79;
 Best Local Similarity 58.8%; Pred. No. 3.9e-24;
 Matches 47; Conservative 8; Mismatches 24; Indels 1; Gaps 1;

QY 4 CMFGNGKGRGKATTGTPCQEWAAQEPHRHSTFPGTKWAGLEKNYCRNPDDING 63
 Db 1 CKTGNGKNTGTMNSKTRGTTGCTQKWSSTSPhR -PFS PATHPSEGLENYCRNPDNGQG 59

RESULT 6
 US-08-612-788-11
 Sequence 11, Application US/08612788
 ; Patent No. 587682

GENERAL INFORMATION:
 / APPLICANT: Folkman, M. Judah
 / O'Reilly, Micheal
 / Cao, Yihai
 / Sim, B. Kim Lee
 / TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 / NUMBER OF SEQUENCES: 45
 / CORRESPONDENCE ADDRESS:
 / APPLICANT: Folkman, M. Judah
 / O'Reilly, Micheal
 / Cao, Yihai
 / Sim, B. Kim Lee
 / TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 / NUMBER OF SEQUENCES: 45
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Jones & Askew
 / STREET: 191 Peachtree Street, 37th Floor
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: U.S.
 / ZIP: 30303-1769
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/612,788
 / FILING DATE:

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 79 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Bovine
 IMMEDIATE SOURCE:
 CLONE: K1
 US-08-612-788-11
 Query Match Score 258.5; DB 3; Length 79;
 Best Local Similarity 57.5%; Pred. No. 2.6e-22;
 Matches 46; Conservative 7; Mismatches 26; Indels 1; Gaps 1;
 QY 4 CMFGNGGTYRKATTVTPCOEWAAQEPHRHSTFPTPNKAGLEKNCRNPDDING 63
 Db 1 CKTGNGGTYRRTAFTKSVTCKWSATSPH-VPKFSPEKFPLAGLENCRNPNDENG 59
 RESULT 8
 US-09-325-11
 / Sequence 11, Application US/09335325
 / Patent No. 6521439
 / GENERAL INFORMATION:
 / APPLICANT: Folkman, M. Judah
 / O'Reilly, Michael
 / Cao, Yihai
 / Sun, B. Kim Lee
 / TITLE OF INVENTION: Angiotatin Fragments and Method of use
 / NUMBER OF SEQUENCES: 45
 / ADDRESSEE: Jones & Askew
 / STREET: 191 Peachtree Street, 37th Floor
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: U.S.
 / ZIP: 30303-1769
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/066,028
 / FILING DATE:
 / CLASSIFICATION:
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: 08/612,788
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Warren, William L.
 / REGISTRATION NUMBER: 36,714
 / REFERENCE/DOCKET NUMBER: 05213-0126
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 404-818-3700
 / TELEX: 404-818-3799
 / INFORMATION FOR SEQ ID NO: 11:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 79 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: <Unknown>
 / TOPOLOGY: linear

MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Bovine
 IMMEDIATE SOURCE:
 CLONE: K1
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-09-333-325-11

Query Match 50.9%; Score 258.5; DB:4; Length 79;
 Best Local Similarity 57.5%; Pred. No. 2.6e-22; Indels 1; Gaps 1;
 Matches 46; Conservative 7; Mismatches 26;

QY 4 CMFGNGKGYRKAKATTGTPCOEWAAQEPHRHSTFIPOTNWKAGLEKNYCRNPDDNG 63
 Db 1 CKTGNGATYRSTTAKTSVTCOKWSATSPTSPH-VPKPSPEKEPLAGLENTCRNPDDNG 59

QY 64 PWCTYMPKLFDFDYLPLIC 83
 Db 60 PWCTYMPDKRYDYLPLIC 79

RESULT 9
 Sequence 1, Application US/09348953
 Patent No. 6538103
 GENERAL INFORMATION:
 APPLICANT: Ji, Richard Wei-Dong
 APPLICANT: Trail, Pamela A.
 TITLE OF INVENTION: LYSINE BINDING FRAGMENTS OF ANGIOSTATIN
 FILE REFERENCE: DB11sequences
 CURRENT APPLICATION NUMBER: US/09/348,953
 CURRENT FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: 60/092,831
 PRIOR FILING DATE: 1998-07-14
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 82
 TYPE: PRT
 ORGANISM: human
 US-09-348-953-1

Query Match 50.9%; Score 258.5; DB:4; Length 82;
 Best Local Similarity 54.3%; Pred. No. 2.7e-22; Indels 1; Gaps 1;
 Matches 44; Conservative 9; Mismatches 27;

QY 3 DCMFNGKGYRKAKATTGTPCOEWAAQEPHRHSTFIPGTNWKAGLEKNYCRNPDDNG 62
 Db 2 ECKTGNGATYRSTTAKTSVTCOKWSSTSPTSPH-PRESPLATHSEGILEENTCRNPDDNG 60

QY 63 GPWCTYMPKLFDFDYLPLIC 83
 Db 61 GPWCTYDPKRYDYLPLIC 81

RESULT 10
 US-08-612-788-8
 Sequence 8, Application US/08612788
 Patent No. 5831682
 GENERAL INFORMATION:
 APPLICANT: Folman, M. Judah
 APPLICANT: O'Reilly, Michael
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta

STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1759
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE:

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 79 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOPOLETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: K1
 US-08-612-788-8

Query Match 50.5%; Score 256.5; DB:2; Length 79;
 Best Local Similarity 55.0%; Pred. No. 4.4e-22; Indels 1; Gaps 1;
 Matches 44; Conservative 8; Mismatches 27;

QY 4 CMFGNGKGYRKAKATTGTPCOEWAAQEPHRHSTFIPGTNWKAGLEKNYCRNPDDNG 63
 Db 1 CKTGNGATYRSTTAKTSVTCOKWSSTSPTSPH-PRESPLATHSEGILEENTCRNPDDNG 59

QY 64 PWCTYMPKLFDFDYLPLIC 83
 Db 60 PWCTYDPKRYDYLPLIC 79

RESULT 11
 US-08-763-528A-2
 Sequence 2, Application US/08763528A
 Patent No. 5854221
 GENERAL INFORMATION:
 APPLICANT: Cao, Yihai
 APPLICANT: Folman, M. Judah
 TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
 TITLE OF INVENTION: and Method of Use
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew, LLP
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: US
 ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/763,528A
 FILING DATE: 12-DEC-1996

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K1
US-09-066-028-8

Query Match Score 256.5; DB 3; Length 79;
Best Local Similarity 55.0%; Pred. No. 4.4e-22;
Matches 44; Conservative 8; Mismatches 27; Indels 1; Gaps 1;
US-08-763-528A-2

Query Match Score 256.5; DB 2; Length 79;
Best Local Similarity 55.0%; Pred. No. 4.4e-22;
Matches 44; Conservative 8; Mismatches 27; Indels 1; Gaps 1;
US-09-066-028-8

Query Match Score 256.5; DB 2; Length 79;
Best Local Similarity 55.0%; Pred. No. 4.4e-22;
Matches 44; Conservative 8; Mismatches 27; Indels 1; Gaps 1;
US-09-066-028-8

RESULT 13
US-09-335-325-8
; Sequence 8, Application US/09335325
; Patent No. 6521439
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; Cao, Yihai
; Sim, B. Kim Lee
; TITLE OF INVENTION: Angiotostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA: US/09/066,028
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear

RESULT 12
US-09-066-028-8
; Sequence 8, Application US/09066028
; Patent No. 6024688
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; Cao, Yihai
; Sim, B. Kim Lee
; TITLE OF INVENTION: Angiotostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; REFERENCE/DOCKET NUMBER: 05213-0126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear

MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: K1
 SEQUENCE DESCRIPTION: SEQ ID NO: 8;
 US-09-335-325-8

Query Match 50.5%; Score 256.5; DB 4; Length 79;
 Best Local Similarity 55.0%; Pred. No. 4.4e-22;
 Matches 44; Conservative 8; Missmatches 27; Indels 1; Gaps 1;

RESULT 14
 US-08-612-788-10
 ; Sequence 10, Application US/08612788
 ; Patent No. 5837882
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, B. Kim Lee
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: U.S.
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; NUMBER OF SEQUENCES: 45
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; CORRESPONDENCE ADDRESS:
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/612,788
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/612,788
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05213-0126
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 79 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; IMMEDIATE SOURCE: Porcine
 ; CLONE: K1
 US-08-612-788-10

Query Match 48.5%; Score 246.5; DB 3; Length 79;
 Best Local Similarity 53.8%; Pred. No. 6e-21;
 Matches 43; Conservative 7; Missmatches 29; Indels 1; Gaps 1;

QY 4 CMFGNGKGYRGKATTGTPQEWAAQEPHRSTFIGTNKWAGLEKNYCRNPDDING 63
 Db 1 CKTGNGKNTRGTTSKSGVTCQKNSVSSH-TPKYSPEKFPLAGLEENYCRNPDDING 59

QY 64 PWCYTMDPKLFDYCDIPIC 83
 Db 60 PWCYTDPETRFDYCDIPIC 79

Query Match 48.5%; Score 246.5; DB 3; Length 79;
 Best Local Similarity 53.8%; Pred. No. 6e-21;
 Matches 43; Conservative 7; Missmatches 29; Indels 1; Gaps 1;

QY 4 CMFGNGKGYRGKATTGTPQEWAAQEPHRSTFIGTNKWAGLEKNYCRNPDDING 63

Wed Oct 1 15:58:48 2003

us-10-088-548-8.sep29.rai

Page 8

Db 1 CKTGKNYRGTTSKSGVTCQKWSYSSPH-IPKYSPEKFPLAGLEENYCRNPDNEKG 59
64 PWCTMNRKLFDYCDIPLC 83
| | | | ; | | | | | | | |
Qy 60 PWCTTDPETRFDYCDIPEC 79
Db

Search completed: September 29, 2003, 08:50:31
Job time : 29 secs

GenCore version 5.1.6
 Copyright (C) 1993 - 2003 Comptech Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2003, 08:49:20 ; Search time 63 Seconds

(without alignments)
 206.546 Million cell updates/sec

Title: US-10-088-548-8

Perfect score: 508

Sequence: 1 EQDCMFNGKNGYRKATTV.....YTMNPRKLFDFCDIPLCASS 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

```

1: /cgn2_6/piodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/piodata/1/pubpaa/US07_PUBCOMB.pep:*
3: /cgn2_6/piodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/piodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/piodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/piodata/1/pubpaa/US05_PUBCOMB.pep:*
7: /cgn2_6/piodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/piodata/1/pubpaa/US09_A_PUBCOMB.pep:*
9: /cgn2_6/piodata/1/pubpaa/US09_A_PUBCOMB.pep:*
10: /cgn2_6/piodata/1/pubpaa/US09_B_PUBCOMB.pep:*
11: /cgn2_6/piodata/1/pubpaa/US09_C_PUBCOMB.pep:*
12: /cgn2_6/piodata/1/pubpaa/US10A_NEW_PUB.pep:*
13: /cgn2_6/piodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/piodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/piodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/piodata/1/pubpaa/US10 NEW_PUB.pep:*
17: /cgn2_6/piodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/piodata/1/pubpaa/US60_PUBCOMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	412	81.1	80	9	US-09-753-064-6	Sequence 6, Appli
2	412	81.1	80	12	US-10-267-137-8	Sequence 8, Appli
3	405	79.7	79	9	US-09-753-064-1	Sequence 1, Appli
4	387	76.2	80	9	US-09-761-120-47	Sequence 47, Appli
5	274.5	54.0	79	9	US-09-761-120-9	Sequence 9, Appli
6	274.5	54.0	79	10	US-09-335-325-9	Sequence 9, Appli
7	274.5	54.0	79	15	US-10-131-241-9	Sequence 9, Appli
8	258.5	50.9	79	9	US-09-761-120-11	Sequence 11, Appli
9	258.5	50.9	79	10	US-09-335-325-11	Sequence 11, Appli
10	258.5	50.9	79	15	US-10-131-241-11	Sequence 2, Appli
11	256.5	50.5	79	9	US-09-753-064-2	Sequence 8, Appli
12	256.5	50.5	79	9	US-09-761-120-8	Sequence 8, Appli
13	256.5	50.5	79	10	US-09-335-325-8	Sequence 8, Appli
14	256.5	50.5	79	12	US-10-267-137-7	Sequence 7, Appli
15	256.5	50.5	79	15	US-10-131-241-8	Sequence 8, Appli

RESULT 1
 US-09-753-064-6
 Sequence 6, Application US/09753064
 Patent No. US2001016544A1

GENERAL INFORMATION:
 APPLICANT: Cao, Yihai
 FOLKMAN, M. JUDAH
 TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor

NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew, LLP
 STREET: 191 Peachtree Street, 37th floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: US

ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/753,064
 FILING DATE: 29-Dec-2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/763,528
 FILING DATE: 12-Dec-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.

REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 0940-0251
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 FEATURE: NAME/KEY: Protein
 LOCATION: 1..80
 OTHER INFORMATION: /note= "Kringle 5 - Figure 3"
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-753-064-6

Query Match 81.1%; Score 412; DB 9; Length 80;
 Best Local Similarity 83.8%; Pred. No. 6..5e-39;
 Matches 67; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 4 CMFGNGKGRKKATVTGTPQEEWAQQEPHRHSTETPGTNKWAGLEKRNCKRNPDQDING 63
 Db 1 CMFGNGKGRKGKATVTGTPQCDWAAQEPHRHSITFPETNPRAGLEKRNCRNPDGVGG 60

Qy 64 PWCYTNNPRKLFDYCDIPLC 83
 Db 1 PWCYTNNPRKLFDYCDVQPC 81
 61 PWCYTNNPRKLFDYCDVQC 80

RESULT 2
 US-10-267-137-8
 ; Sequence 8, Application US/10267137
 ; Publication No. US2003014850A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xin, Li
 ; APPLICANT: Li, Zai-Ping
 ; APPLICANT: Gan, Ren-bao
 ; APPLICANT: Zhou, Qing-wei
 ; APPLICANT: Xu, Ren
 ; TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCYTE
 ; TITLE OF INVENTION: GROWTH FACTOR AND USES THEREFOR
 ; FILE REFERENCE: 524202000100
 ; CURRENT APPLICATION NUMBER: US/10/267,137
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: 60/328,329
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 80
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence alignment of kringle domains of
 ; other information: Plasminogen and FGF
 ; US-10-267-137-8

Query Match 81.1%; Score 412; DB 12; Length 80;
 Best Local Similarity 83.8%; Pred. No. 6..5e-39;
 Matches 67; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

RESULT 4
 US-09-761-120-47
 ; Sequence 47, Application US/09761120
 ; Patent No. US2003037847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: Folkman, Michael
 ; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmin
 ; FILE REFERENCE: 09940-0151 (33171-25068)
 ; CURRENT APPLICATION NUMBER: US/09/7761,120
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: 09/309,821
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 08/866,735
 ; PRIOR FILING DATE: 1997-05-30

Qy 4 CMFGNGKGRKKATVTGTPQEEWAQQEPHRHSTETPGTNKWAGLEKRNCKRNPDQDING 63
 Db 1 CMFGNGKGRKGKATVTGTPQCDWAAQEPHRHSITFPETNPRAGLEKRNCRNPDGVGG 60

Qy 64 PWCYTNNPRKLFDYCDIPLC 83
 Db 1 PWCYTNNPRKLFDYCDVQPC 81
 61 PWCYTNNPRKLFDYCDVQC 80

RESULT 3
 US-09-753-064-1
 ; Sequence 1, Application US/09753064
 ; Patent No. US2001001664A1

```

i NUMBER OF SEQ ID NOS: 47
i SOFTWARE: PatentIn version 3.0
i SEQ ID NO: 47
i LENGTH: 80
i TYPE: PRT
i ORGANISM: Murinae gen. sp.
i OTHER INFORMATION: Kringle 5
i US-09-761-120-47

Query Match 76.2% ; Score 387; DB 9; Length 80;
best Local Similarity 80.0%; Pred. No. 4.2e-36;
Matches 64; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 4 CMFGNGKGYRKAKATTGTPCQEAQAQPHEFHSTEFPGINKWAGLEKKNYCNPDPDING 63
Db 1 CTTGNGNTRGMSSTRGTTCTGWSSTSPLR-PTFSRSPATHSEGLENQCRNDGQG 60

QY 64 PRCYTMNPKRLFEDYCDPLC 83
Db 61 PRCYTMNPKRLYCD-PLC 80

RESULT 5
US-09-761-120-9
i Sequence 9, Application US/09761120
i Patent No. US20020037347A1
i GENERAL INFORMATION:
i ; APPLICANT: Folkman, M. Judah
i ; APPLICANT: O'Reilly, Michael
i ; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
i ; FILE REFERENCE: 0940-0111 (43171-250668)
i ; CURRENT APPLICATION NUMBER: US/09761,120
i ; PRIORITY DATE: 2001-01-16
i ; PRIOR APPLICATION NUMBER: 09/309,821
i ; PRIOR FILING DATE: 1999-05-11
i ; PRIOR APPLICATION NUMBER: 08/866,735
i ; PRIOR FILING DATE: 1997-05-30
i ; NUMBER OF SEQ ID NOS: 47
i ; SOFTWARE: PatentIn version 3.0
i ; SEQ ID NO: 9
i ; LENGTH: 79
i ; TYPE: PRT
i ; ORGANISM: Macaca sp.
i ; FEATURE:
i ; NAME/KEY: misc_feature
i ; OTHER INFORMATION: Kringle 1
i US-09-761-120-9

Query Match 54.0% ; Score 274.5; DB 9; Length 79;
Best Local Similarity 58.8%; Pred. No. 1.7e-23;
Matches 47; Conservative 8; Mismatches 24; Indels 1; Gaps 1;

QY 4 CMFGNGKGYRKAKATTGTPCQEAQAQPHEFHSTEFPGINKWAGLEKKNYCNPDPDING 63
Db 1 CTTGNGNTRGMSSTRGTTCTGWSSTSPLR-PTFSRSPATHSEGLENQCRNDGQG 59

QY 64 PRCYTMNPKRLFEDYCDPLC 83
Db 60 PRCYTMNPKRLYCD-PLC 79

RESULT 6
US-09-335-325-9
i Sequence 9, Application US/09335325
i ; Patent No. US20020164717A1
i GENERAL INFORMATION:
i ; APPLICANT: Folkman, M. Judah
i ; O'Reilly, Michael
i ; Cao, Yihai
i ; Sim, B. Kim Lee
i ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use

```

PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Rhesus monkey
; US-10-131-241-9

RESULT 8
US-09-761-120-11
; Sequence 11, Application US/09761120
; Patent No. US2002003747A1

GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT APPLICATION NUMBER: US/09/7761,120
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS:
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Bos sp.
; FEATURE:
; NAME/KEY: mIsc.Feature
; OTHER INFORMATION: Kringle 1
; US-09-761-120-11

Query Match 54.0%; Score 274.5; DB 15; Length 79;
Best Local Similarity 58.8%; Pred. No. 1.7e-23;
Matches 47; Conservative 8; Mismatches 24; Indels 1; Gaps 1;

Qy 4 CMFGNGKGYRKAKATTVGTGTPCOEWAQEPHRHSTFIPGTNWKAGLEKNYCRNPDDGNG 63
Db 1 CKTGNGKNTGTMSTKTRGTTQKWSSTSHER-PTFSPATHPSEGLENYCRRNPNDGQG 59

Qy 64 PWCYTANPKLFDYCDIPLC 83
Db 60 PWCYTIDPDKRYDCIPLC 79

RESULT 9
US-09-335-325-11
; Sequence 11, Application US/09335325
; Patent No. US2002003747A1

GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Micheal
; Cao, Yihui
; Sim, B. Kim Lee
; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45

PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID Nos: 65
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Bovine
; US-10-131-241-11

Query Match Score 50.9%; Best Local Similarity 57.5%; Pred. No. 1..1e-21;
 Matches 46; Conservative 7; Mismatches 26; Indels 1; Gaps 1;

QY 4 CMFGNGKGRGKATTGTCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGING 63
 Db 1 CKTGNGNYRGTMSKTKNITCQWSSTSFR-PFSPATHPSEGLENCRNPNDPG 59

Query Match Score 258.5; DB 15; Length 79;
 Best Local Similarity 57.5%; Pred. No. 1..1e-21;
 Matches 46; Conservative 7; Mismatches 26; Indels 1; Gaps 1;

QY 64 PWCTMNPRLFDYCDIPLC 83
 Db 60 PWCTTDPDKRYDCIPLC 79

RESULT 12
 US-09-761-120-8

Sequence 8, Application US/09761120
 ; Patent No. US2000037847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmi

FILE REFERENCE: 05940-0151 (43171-252068)
 CURRENT APPLICATION NUMBER: US/09/761,120
 PRIORITY APPLICATION NUMBER: 09/309,821
 PRIOR FILING DATE: 1999-05-11
 PRIORITY NUMBER: 08/866,735
 PRIORITY FILING DATE: 1997-05-30
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 8
 LENGTH: 79
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Kringle 1

US-09-761-120-8

Query Match Score 50.5%; Best Local Similarity 55.0%; Pred. No. 1..8e-21;
 Matches 44; Conservative 8; Mismatches 27; Indels 1; Gaps 1;

QY 4 CMFGNGKGRGKATTGTCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGING 63
 Db 1 CKTGNGNYRGTMSKTKNITCQWSSTSFR-PFSPATHPSEGLENCRNPNDPG 59

Query Match Score 256.5; DB 9; Length 79;
 Best Local Similarity 55.0%; Pred. No. 1..8e-21;
 Matches 44; Conservative 8; Mismatches 27; Indels 1; Gaps 1;

QY 64 PWCTMNPRLFDYCDIPLC 83
 Db 60 PWCTTDPDKRYDCIPLC 79

RESULT 13
 US-09-335-325-8

Sequence 8, Application US/09335325
 ; Patent No. US20020164717A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; O'Reilly, Michael Cao, Yihai Sim, B. Kim Lee
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/753,064
 ; FILING DATE: 29-Dec-2000
 ; CLASSIFICATION: <unknowm>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/763,528
 ; FILING DATE: 12-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 05940-0251
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 79 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..79
 ; OTHER INFORMATION: /note= "Kringle 1 - Figure 3"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/335,325
 FILING DATE: 17 Jun 1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warter, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 79 amino acids
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: KI
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-335-325-8

Query Match 50.5%; Score 256.5; DB:10; Length 79;
 Best Local Similarity 55.0%; Pred. No. 1.8e-21;
 Matches 44; Conservative 8; Mismatches 27; Indels 1; Gaps 1;

Qy 4 CMFGNGKGYRGKKATTVTPCQEWAAQEPHRHSTPQTNKWAGLEKNYCRNPGDING 63
 Db 1 CKTGNGNYRTGMSKTKITCQKWSSTSPhR-PRESATHPSSEGLENICRNFDNDFQG 59

Query Match 50.5%; Score 256.5; DB:15; Length 79;
 Best Local Similarity 55.0%; Pred. No. 1.8e-21;
 Matches 44; Conservative 8; Mismatches 27; Indels 1; Gaps 1;

Qy 4 CMFGNGKGYRGKKATTVTPCQEWAAQEPHRHSTPQTNKWAGLEKNYCRNPGDING 63
 Db 1 CKTGNGKYRGMSKTKITCQKWSSTSPhR-PRESATHPSSEGLENICRNFDNDFQG 59

RESULT 14
 US-10-267-137-7
 ; Sequence 7, Application US/10267137
 ; GENERAL INFORMATION:
 ; APPLICANT: Xin, Li
 ; APPLICANT: Li, Zai-Ping
 ; APPLICANT: Gan, Ren-bao
 ; APPLICANT: Zhou, Qing-wee
 ; APPLICANT: Xu, Ren
 ; TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCYTE
 ; FILE REFERENCE: 52A28200100
 ; CURRENT APPLICATION NUMBER: US/10/267,137
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: 60/328,329
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 7
 ; LENGTH: 79
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Sequence alignment of kringle domains of

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

M protein - protein search, using sw model

run on: September 29, 2003, 08:44:24 ; Search time 39 Seconds
 (without alignments)
 212,064 Million cell updates/sec

title: US-10-088-548-8
 exact score: 508
 sequence: 1 EQDCMFNGKGYRKATTV.....YTMNPRKLFDYCDIPLCASS 86

scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 283308 seqs, 9616882 residues

total number of hits satisfying chosen parameters: 29185

minimum DB seq length: 0
 maximum DB seq length: 86

post-processing: Maximum Match 0%
 Listing first 45 summaries

database :	Score	Query	Match	Length	DB	ID	Description
	54.5	PTR_76;*	1	64	WDSR5L		neurotoxin V - Egg
	54.5	pir1;*	1	65	EB3078		conserved hypothetical protein
	52.5	pir2;*	1	64	WDSR5M		neurotoxin V - scorpion
	51.0	pir3;*	1	65	TC32082		hypothetical protein
	49.5	pir4;*	1	68	GB81600		hypothetical protein
	49.5	pir5;*	1	65	NTSREB		neurotoxin XI - scorpion
	48.5	pir6;*	1	65	PQ0852		glycoprotein H -
	48.5	pir7;*	1	40	T5510		hypothetical protein
	47.5	pir8;*	1	59	S21332		hypothetical protein
	47.5	pir9;*	1	67	DB1186		hypothetical protein
	47.5	pir10;*	1	59	T62P5J		mambin - eastern
	47.0	pir11;*	1	9.3	77	A02564	hypothetical protein
	47.0	pir12;*	1	9.3	51	AR3350	hypothetical protein
	46.5	pir13;*	1	9.2	62	A69034	hypothetical protein
	46.5	pir14;*	1	9.2	73	F33824	hypothetical protein
	46.5	pir15;*	1	9.2	86	T17313	hypothetical protein
	46.5	pir16;*	1	9.1	71	A34768	ORF1 protein - Ori
	46.0	pir17;*	1	9.1	65	P00850	hypothetical protein
	45.5	pir18;*	1	9.0	65	PQ0848	glycoprotein H -
	45.5	pir19;*	1	9.0	65	A02631	hypothetical protein
	45.5	pir20;*	1	9.0	65	G61561	hypothetical protein
	45.0	pir21;*	1	8.9	46	A33940	neurotoxin alpha-1
	45.0	pir22;*	1	8.9	80	E97800	embryogenic callus
	44.5	pir23;*	1	8.9	50	E02529	toxin CSTX-1
	44.5	pir24;*	1	8.8	62	A61561	insect toxin
	44.5	pir25;*	1	8.7	64	A33940	alpha-1
	44.0	pir26;*	1	8.7	69	T14285	embryogenic callus
	44.0	pir27;*	1	8.7	74	A513356	toxin CSTX-1
	44.0	pir28;*	1	8.7	85	A33940	insect toxin
	44.0	pir29;*	1	8.7	85	T14285	embryogenic callus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: GB6500
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-68 <STM>
A;Cross-references: GB:AE004025; GB:AE003849; NID:9107217; PIDN:AAF84897.1; GSPDB:GN
R;Simpson, A.J.S.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrier
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.P.; Kuramae, E.E.; La
chado, M.A.; Madeira, C.L.; Marinho, C.F.M.; Marques, M.V.; Martins
C;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; Santelli, R.V.; Sawa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; da Silva Jr., W.A.; da Silv
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A;Content: annotation: A59328
C;Genetics:
A;Gene: XF2098

Query Match 9.7% Score 49.5; DB 2; Length 68;
Best Local Similarity 31.6%; Pred. No. 1.8e+02
Matches 12; Conservative 3; Mismatches 6; Indels 17; Gaps 2;

Qy 65 WCYTANPR-----KLEDY----CDIPLCAS 85
Db 5 WCYQGSTRAATSELQELRLQQYAASEMSCALIPLCAS 42

RESULT 6
NTSRB neurotoxin XI - scorpion (Buthus occitanus)
C;Species: Buthus occitanus tunelanus
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 23-Aug-1996
C;Accession: A01746
R;Martin, M.E.; Rochat, H.
Toxicon 22, 279-291, 1984
A;Title: Purification of thirteen toxins active on mice from the venom of the North A
C;Reference number: A94316; PMID:84224814; PMID:6729843
A;Accession: A01746
A;Molecule type: protein
A;Residues: 1-65 <MDA>
C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin; venom
F;12-63,16-36,22-46,26-48/Disulfide bonds: *status experimental
F;64/Modified site: blocked carboxyl end (Asn) (probably amidated) #status experimental

Query Match 10.3% Score 52.5; DB 1; Length 64;
Best Local Similarity 36.4%; Pred. No. 81;
Matches 16; Conservative 3; Mismatches 14; Indels 11; Gaps 3;

Qy 38 TRIPGDN-----KWAQLEKNYCR-NPQGDINGPQYTYANPR 72
Db 13 TFFCGRNAYCDDECKKGGESEGYCQWASPIG--NACWCYKLPDFR 54

RESULT 4
T03052 hypothetical protein 065L - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Accession: T03082
C;Sequence: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03082
R;Bair, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1991
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: 214834; PMID:98141633; PMID:9482589
A;Status: Preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-65 <BAH>
A;Cross-references: EMBL:AF003534; NID:92738385; PIDN:AAF94456.1; PMID:92738429

Query Match 10.0% Score 51; DB 2; Length 65;
Best Local Similarity 29.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 4; Mismatches 19; Indels 16; Gaps 2;

Qy 39 FPGTGNWGLEKVKCRAPFDGTDINGPWCY-----TMNPKLFDDYDIPLC 83
Db 14 FVLTNVFAFPDGMCNLNDGSVGGCVRVESPITTKN----YCDYYC 62

RESULT 5
GB2600 hypothetical protein XF2098 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Accession: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82000
R;Anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 408, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; PMID:20365717; PMID:10910347
A;Content: annotation: A59328
A;Accession: PQ0852
A;Molecule type: DNA
A;Residues: 1-65 <GO4>
A;Experimental source: strain C4

A;Accession: PQ0851
A;Molecule type: DNA
A;Residues: 1-65 <GOM1>
A;Experimental source: isolate C3
A;Accession: PQ0054
A;Molecule type: DNA
A;Residues: 1-65 <GOM2>
A;Experimental source: isolate C9
A;Accession: PQ0853
A;Molecule type: DNA
A;Residues: 1-65 <GO2>
A;Experimental source: strain C6
C;Superfamily: hepesvirus glycoprotein H
C;Keywords: glycoprotein; membrane protein

Query Match 9 5%; Score 48.5; DB 2; Length 65;
Best Local Similarity 20.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 9; Mismatches 18; Indels 29; Gaps 4;

Qy 23 TPCQWAAQEPHRHSTFIPGTNKGLEYKNCRNPDDINGPWC-----YTMNRK 73
Db 12 TPCYSW-----RFWTISNEHCKN--GNSENPIVRRPQFITNFYTKNDIR 54

Qy 74 LFDYCDPLC 83
Db 55 IV--QVPKC 61

RESULT 8

hypothetical protein SC6G10_01c - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35510
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21581
A;Accession: T35510
A>Status: Preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA
A;Residues: 1-40 <SEED>
A;Cross-references: EMBL:AL049497; PIDN:GAB39855.1; GSPDB:GN000070; SCOEDB:SC6G10_01c
A;Experimental source: strain A3(2)
C;Genetics:

Query Match 9 4%; Score 48; DB 2; Length 40;
Best Local Similarity 47.8%; Pred. No. 1.5e+02;
Matches 11; Conservative 2; Mismatches 6; Indels 4; Gaps 1;

Qy 21 TGPQCQWAAQEPHRHSTFIPGT 43
Db 7 SGTPHRAANPPPHRH----PGT 25

RESULT 9

hypothetical protein 2 - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jun-2001
R;Paulus, F.; Canada, J.; Otten, L.
submitted to the EMBL Data Library, October 1990
A;Reference number: S21331
A;Accession: S21332
A>Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-59 <PAU>
A;Cross-references: EMBL:X55055; PIDN:CAA38901.1; PID:g39140

Query Match 9 4%; Score 47.5; DB 2; Length 59;
Best Local Similarity 31.1%; Pred. No. 2.6e+02;

Matches 14; Conservative 4; Mismatches 16; Indels 11; Gaps 2;

Qy 22 GTPCQWAAQEPHRHSTFIPGTNKGLEYKNCR-NFDGDDINGPW 65
Db 16 GSPAEPPSSRPHRS-----AGLLIVYRPRSSSPTHAAW 50

RESULT 10

hypothetical protein NMB0542 (imported) - *Neisseria meningitidis* (strain MC58 serogroup C)
C;Species: *Neisseria meningitidis*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81186
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, B.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischman, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masinpani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Mozon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; PMID:20175755; PMID:10710307
A;Accession: D81186
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <TET>
A;Cross-references: GB:AE002410; GB:AE002098; NID:97225766; PMID:AAF40971.1; PMID:97225766
A;Experimental source: serogroup B, strain MC58
C;Generics:
A;Gene: NM005442

Query Match 9 4%; Score 47.5; DB 2; Length 67;
Best Local Similarity 29.0%; Pred. No. 2.9e+02;
Matches 9; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

Qy 41 PGTKWAGLEKNY--CRNPGDINGPWCYT 68
Db 23 PGNEQWNGHPVRLPELEGESGSVACPYCGT 53

RESULT 11

"68P5J
mambin - eastern Jameson's mamba
N;Alternative names: dendroaspis short toxin S5C1
C;Species: Dendroaspis jamesoni kaimosse [eastern Jameson's mamba]
C;Date: 19-Feb-1984 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A42561; SS0910; A16183
R;McDonnell, R.S.; Dennis, M.S.; Louie, A.; Shuster, M.; Mulkeirin, M.G.; Lazarus, R.
Biochemistry 31, 4764-4772, 1992
A;Title: Mambin, a potent glycoprotein IIB-IIIa antagonist and platelet aggregation :
A;Reference number: A42561; PMID:92273586; PMID:1591238
A;Accession: A42561
A;Molecule type: protein
A;Residues: 1-59 <ICD>
A;Cross-references: PIDN:AB22225.1; PMID:g249694

A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:104347)
R;Jaseja, M.; Lu, X.; Williams, J.A.; Sutcliffe, M.J.; Kakkar, V.V.; Parslow, R.A.;
Eur. J. Biochem. 226, 861-868, 1994
A;Title: (1)H-NMR assignments and secondary structure of dendroaspin, an RGD-contain:
A;Reference number: S50910; PMID:95112651; PMID:7813476
A;Accession: S50910
A;Molecule type: protein
A;Residues: 1-59 <IAMS>
R;Zoubert, F.J.; Talaard, N.; Biophys. Acta 579, 226-233, 1979
A;Title: Some properties and the complete primary structures of two reduced and S-ca:
A;Reference number: A90630; PMID:79232598; PMID:465532
A;Accession: A01683
A;Molecule type: protein
A;Residues: 1-15, CT, 18-27, 'RNI', 28-32, 34-59 <JOU>
C;Comment: The cell attachment motif may serve in inhibiting platelet aggregation.
C;Superfamily: snake toxin
C;Keywords: toxin; venom
F;43-45/Region: cell attachment (R-G-D) motif

F;3-22,17-37,39-51,52-57/disulfide bonds: #status Predicted

Query Match 9.3%; Score 47; DB 1; Length 59;
Best Local Similarity 30.5%; Pred. No. 2.9e+0;
Matches 18; Conservative 3; Mismatches 14; Indels 24; Gaps 4;

Qy 15 KKATVVTGTPCQE-----WAQQEPHRHSTFPGTNKWALEKNCRNPDGDINGPWC 66
Db 10 KRPTEBT--CQDPSCKNIN-----TDFNIIRKGCC-----CTPPRGDMPSYIC 51

RESULT 12

AF2564 hypothetical protein asr8513 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120de

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AF2564

R;Keneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchii, N.; Nakazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; PMID:21595255; PMID:11759840

A;Accession: AF2564

A;Status: preliminary

A;Molecule type: DNA

A;Cross references: GB:AP003604; PMID:3AB77432.1; PID:517134876; GSDB:GN00183

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: asr8513

A;Genome: plasmid

Query Match 9.3%; Score 47; DB 2; Length 77;
Best Local Similarity 33.3%; Pred. No. 3.8e+0;
Matches 9; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 40 TPGTNKWALEKNCRNPDGDINGPWC 66
Db 40 VKGTCRHPGSPVGFCPCNDGTSSGPYC 66

RESULT 13

AF3350 hypothetical protein BMET07088 [Imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A;Reference number: AD3252; PMID:11756688

A;Status: preliminary

A;Molecule type: DNA

A;Cross references: GB:AE008917; PMID:AN51969.1; PID:917982729; GSDB:GN00190

A;Experimental source: strain 16M

A;Gene: BMET07088

A;Map Position: I

Query Match 9.2%; Score 46.5; DB 2; Length 51;
Best Local Similarity 31.4%; Pred. No. 2.9e+0;
Matches 11; Conservative 4; Mismatches 13; Indels 7; Gaps 1;

Qy 24 PCOBWAQEQPHRHSTFPGTNKWALEKNCRNPD 58
Db 5 PCTDAGHERPRRSS-----AHKATNCRRE 32

DT	15-SEP-2003 (Rel. 42, Created)	OX	NCBI_TaxID=6494;
DT	15-SEP-2003 (Rel. 42, Last sequence update)	RN	[1]
DT	15-SEP-2003 (Rel. 42, Last annotation update)	RP	SEQUENCE FROM N.A.
DE	Hypothetical zinc-binding UPF0243 protein vc2429.	RC	TISSUE=Venom duct;
GN	VC2429.	RX	MEDLINE=20037955; PubMed=10573284;
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.	RA	Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
OC		RT	"Conopeptides from Conus striatus and Conus textile by cDNA cloning.";
OA		RT	Peptides 20:1139-1144 (1999).
RN		RL	-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By similarity).
RP	SEQUENCE FROM N.A.	CC	-!- SUBCELLULAR LOCATION: Secreted (By similarity).
RC	STRAIN=El FOR N16961 / Serotype O1;	CC	-!- TISSUE SPECIFICITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS OMEGA-TYPE FAMILY.
RX	MEDLINE=10406833; PubMed=10952201;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA	Heidelberg J.F., Elsner J.A., Nelson W.C., Clayton R.A., Gwynn M.L., Dodson R.J., Hickey D.H., Peterson J.D., Unayam L.A., Gill S.R., Neilson K.E., Read T.D., Tettelin H., Richardson D., Brumley M.D., Vanatherwa J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., McAlanous J.J., Venter J.C., Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	CC DR AF146359; ADD31919.1; DR InterPro:IPR00214; Conotoxin.
RA	Dodson R.J., Haff D.H., Hickey E.K., Peterson J.D., Unayam L.A., Gill S.R., Neilson K.E., Read T.D., Tettelin H., Richardson D., Brumley M.D., Vanatherwa J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., McAlanous J.J., Venter J.C., Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	DR Pfam:PF02950; Conotoxin; 1. KW Calcium; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor; Signal. CC FT SIGNAL 1 22 BY SIMILARITY.
RA	Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	CC FT PROPEP 23 50 BY SIMILARITY.
RA	Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	CC FT PEPTIDE 51 82 BY SIMILARITY.
RA	Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	CC FT DISUFID 53 71 BY SIMILARITY.
RA	Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	CC FT DISUFID 60 76 BY SIMILARITY.
RA	Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	CC FT DISUFID 70 81 BY SIMILARITY.
RA	Fraser C.M.; RT DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;	CC	CC SQ SEQUENCE 82 AA; 9305 MW; 1739D2531B865860 CRC64;
CC		CC	Query Match Score 10.7%; Best Local Similarity 30.8%; Matches 12; Length 82; Pred. No. 19; Conservative 4; Mismatches 6; Indels 17; Gaps 1; Gaps 1;
CC		CC	QY 47 AGIJEKNCRNPDDINGPCYTANPRKFDYCDPLCAS 85
CC		CC	DB 46 AKLEKNIC-----QEKWDICPVFLGS 67
CC		RESULT 4	RESULTS
CC		CC SCX5_ANNDMA STANDARD PRT; 64 AA.	SCX5_ANNDMA STANDARD PRT; 64 AA.
CC		CC ID SCX5_ANNDMA STANDARD PRT; 64 AA.	ID SCX5_ANNDMA STANDARD PRT; 64 AA.
CC		CC AC P01422; DR 21-JUL-1986 (Rel. 01, Created)	AC P01422; DR 21-JUL-1986 (Rel. 01, Last sequence update)
CC		CC FT METAL 10 ZINC (BY SIMILARITY).	FT METAL 10 ZINC (BY SIMILARITY).
CC		CC FT METAL 13 ZINC (BY SIMILARITY).	FT METAL 13 ZINC (BY SIMILARITY).
CC		CC FT METAL 29 ZINC (BY SIMILARITY).	FT METAL 29 ZINC (BY SIMILARITY).
CC		CC FT METAL 33 ZINC (BY SIMILARITY).	FT METAL 33 ZINC (BY SIMILARITY).
CC		CC SQ SEQUENCE 65 AA; 7397 MW; 2ED887CLD1D8AD90 CRC64;	SQ SEQUENCE 65 AA; 7397 MW; 2ED887CLD1D8AD90 CRC64;
CC		CC Query Match Score 10.7%; Best Local Similarity 31.7%; Matches 20; Length 65; Pred. No. 15; Conservative 2; Mismatches 24; Indels 17; Gaps 3;	Query Match Score 10.7%; Best Local Similarity 31.7%; Pred. No. 15; Length 65; Pred. No. 19;保守性 2; 错配 24; 插入/删除 17; 缺口 3;
CC		CC QY 15 KRATIVGTPC--QWVAQOEPHHSFIFPITNK----WAGGEKKNCRPDGDIN 62	QY 15 KRATIVGTPC--QWVAQOEPHHSFIFPITNK----WAGGEKKNCRPDGDIN 62
CC		CC DB 28-FEB-2003 (Rel. 41, Last annotation update)	DB 28-FEB-2003 (Rel. 41, Last annotation update)
CC		CC DE Omega-type conotoxin Tx06 precursor.	DE Neurotoxin V (AaH5).
CC		CC GN TX06.	OS Androctonus mauretanicus (Scorpion). Fukaoyots; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones; CC Buthidae; Buthidae; Androctonus; OC Buthidae; Buthidae; Androctonus; OX NCBI_TaxID=6660;
CC		CC RN [1]	RN [1]
CC		CC RP SEQUENCE.	RP SEQUENCE.
CC		CC RC TISSUE=Venom;	RC TISSUE=Venom;
CC		CC RX MEDLINE=55192276; PubMed=3992595;	RX MEDLINE=55192276; PubMed=3992595;
CC		CC RA ROSSO J.P., Rochat H.;	RA ROSSO J.P., Rochat H.;
CC		CC RT "Characterization of ten proteins from the venom of the Moroccan scorpion Androctonus mauretanicus, six of which are toxic to the mouse."	RT "Characterization of ten proteins from the venom of the Moroccan scorpion Androctonus mauretanicus, six of which are toxic to the mouse."
CC		CC RL Toxicon 23:113-125(1985).	RL Toxicon 23:113-125(1985).
CC		CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channel, thereby blocking neuronal transmission.	-!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channel, thereby blocking neuronal transmission.
CC		CC -!- SUBCELLULAR LOCATION: Secreted.	-!- SUBCELLULAR LOCATION: Secreted.
CC		CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.	-!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC		CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.	-!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC ALPHA-TOXIN SUBFAMILY.
DR PIR; A01742; NTSR5M.
DR HSSP; P01484; JAH0.
DR InterPro; IPR003614; Knot1.
DR InterPro; IPR001219; Neurotoxin.
DR InterPro; IPR0012061; Scorpion_toxinL.
DR Pfam; PF00537; toxin_3_1.
DR PRINTS; PRO0284; TOXIN_PDF00908; Scorpion_toxinL_1.
DR SMART; SM00505; Knot1.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
KW Amidation.
FT 63 BY SIMILARITY.
DISULFID 12 36 BY SIMILARITY.
DISULFID 16 46 BY SIMILARITY.
DISULFID 22 48 BY SIMILARITY.
DISULFID 26 64 AMIDATION.
MOD RES 64 SEQUENCE 64 AA; 7301 MW; 3D03A733534CD866 CRC64;

Query Match 10.3%; Score 52.5%; DB 1; Length 64;
Best Local Similarity 36.4%; Prod. No. 25; Gaps 3;
Matches 16; Conservative 3; Mismatches 14; Indels 11; Gaps 3;

QY 38 TPIPGTN-----KWAIGLEKNYCR--NPDDGINDPGCYTMNPR 72
Db 13 TPCGGRNAYCDDECKRKKGEGSEGYCQWASPTG--NACWCKYLDR 54

RESULT 5
GBGD_HUMAN
ID GBGD_HUMAN STANDARD; PRT; 67 AA..
AC Q9PWN3; Q8ULJ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB Guanine nucleotide-binding protein G(1)/G(S)/G(O) gamma-13 subunit.
GN GNG13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20040713; PubMed=10570481;
RA Huang L.; Shanker Y.G.; Dubauskaitė J.; Zheng J.Z.; Yan W.,
RA Rosenzweig S.; Spielman A.I.; Max M.; Margolskee R.F.;
RT Gramm13 colocalizes with gustducin in taste receptor cells and
RT mediates IP3 responses to bitter denatonium.ⁿ
RN [2]
RP SEQUENCE FROM N.A.
RA Inoue S.; Sano H.; Ohta M.;
RT E.coli toxicity assay: a novel expression screening method for
RT isolation of mammalian genes with membrane-associated domains or ATP
RT binding/ATPase domains.
RN [3]
RP SEQUENCE FROM N.A.
RA Puh H.L.; ILLI; Ikeda S.R.; Aronstam R.S.;
RL Submitted (MUR 2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Frankland J.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.

CC -!- SUBUNIT: G proteins are composed of 3 units (alpha, beta and gamma).

CC -!- SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; AY029486; AAK0260; 1;
DR EMBL; AB030307; BAA2768; 1;
DR EMBL; AB006465; AAK61257; 1;
DR EMBL; AF493880; AAM12594; 1;
DR AL031033; CAB3059; 1; ALT_INIT.
DR Genew; HGNC:14131; GNG13.
DR MIM; 607298;
DR InterPro; IPR01770; G-gamma.
DR Pfam; PF00631; G-gamma; 1;
DR PRINTS; PR00321; GPROTEIN_G.
DR ProDom; PD003783; G-gamma; 1;
DR SMART; SM0024; GGL; 1.
DR PROSITE; PS50058; G_PROTEIN_GAMMA; 1.
KW Transducer; Lipoprotein; Multigene family.
FT LIPID 64 64 FARNESYL (BY SIMILARITY);
SQ PROPEP 65 67 REMOVED IN MATURE FORM (BY SIMILARITY);
SEQUENCE 67 AA; 7949 MW; 080E0C4A8E70327 CRC64;

Query Match 9.6%; Score 49; DB 1; Length 67;
Best Local Similarity 41.9%; Prod. No. 64;
Matches 13; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

QY 37 STTIPGTINKWA-GLEKKNYCRNPDDGINDNGPWR 65
Db 28 SKTIPELLKWKEDG2PKDPFLNDLMNNPPW 58

RESULT 6
GBGD_MOUSE
ID GBGD_MOUSE STANDARD; PRT; 67 AA..
AC Q9JMF3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-13 subunit.
GN GNG13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TAXID=10900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=11036910; PubMed=11157797;
RA Daniels R.J.; Peden J.F.; Lloyd C.; Horsley S.W.; Clark K.,
RA Tufarelli C.; Kearney L.; Buckle V.J.; Doggett N.A.; Flint J.,
RA Biggs D.R.;
RT Sequence and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.^t
RN [4]
RP SEQUENCE FROM N.A.
RA Puh H.L.; ILLI; Ikeda S.R.; Aronstam R.S.;
RL Submitted (MUR 2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Frankland J.;

RP SEQUENCE FROM N.A.
RX MEDLINE=20145471; PubMed=10679242;
RA Inoue S.; Sano H.; Ohta M.;
RT "Growth suppression of Escherichia coli by induction of expression of

mammalian genes with transmembrane or ATPase domains.";

RT Biochem. Biophys. Res. Commun. 268:553-561(2000).

RL [3]

RP SEQUENCE FROM N.A.

RC STRAIN=557BL6J; TISSUE=Cerebellum;

RX MEDLINE=1085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Furukoshi Y., Konno H., Adachi J., Fukuda S., Izawa K., Izawa M., Nishi K., Kiyosawa H., Yamamoto I., Saito T., Okazaki Y., Gotohori T., Bono H., Kasikawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesce G., Quackenbush J., Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner U., Washio T., Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiyama M., Lyons P., Marchionni L., Mashima J., Mazzaelli J., Montaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Scheibenbach C., Seye T., Shibata Y., Storch K.-T., Suzuki H., Togyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Yashizaki K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

RT "Functional annotation of full-length mouse cDNA collection.";

RL RNAME=65-650(2001).

CC -!- FUNCTION: GRANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALLING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.

CC -!- SUBUNIT: G proteins are composed of 3 units (alpha, beta and gamma).

CC -!- SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL: AX029481; AAC4268.1; -.

CC DR EMBL: AB030194; BAA9275.1; -.

CC DR MBD: AK018778; BAB3103.1; -.

CC DR MGI: 1925616; Gng13.

CC DR GO:0005834; C: heterotrimeric G-protein complex; IPI: GO:0003921; F: heterotrimeric G-protein activity; IPI: GO:0007200; P:G-protein signaling, coupled to IP3 second . . ; IDA.

CC DR InterPro: IPR001770; G gamma.

CC DR PRINTS: PF00631; G-gamma; 1.

CC DR PRODOM: DD00321; GPROTEIN.

CC DR SMART: SM00224; GSI; 1.

CC DR PROSITE: PS50058; G-PROTEIN GAMMA; 1.

CC KW Transducer; Penetrin; Lipoprotein; Multigene family; FARNESYL (BY SIMILARITY).

CC FT LIPID 64 64 REMOVED IN NATURE FORM (BY SIMILARITY).

CC FT PROPEP 65 67 REMOVED IN NATURE FORM (BY SIMILARITY).

CC SQ SEQUENCE 67 AA; 7979 MW; 1FB8074EB5CB50F5 CRC64;

CC Query Match 9.6%; Score 49; DB 1; Length 67; Best Local Similarity 41.9%; Pred No. 64; Indels 2; Gaps 1; matches 13; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

CC QY 37 STFPGTNKWA-GLEKNYCRNPDGDINGPW 65

CC DB 28 SKTIPELLKWIENGIPDPFLNPDLNMKNWW 58

CC RESULT 8 SCX_BUOC SCXB_BUOC STANDARD PRT; 65 AA.

CC ID SCXB_BUOC AC 21-JUL-1986 (Rel. 01, Crested)

CC DT 21-JUL-1986 (Rel. 01, Last sequence update)

CC ID SCXB_BUOC AC 28-FEB-2003 (Rel. 41, Last annotation update)

CC DE Neurotoxin XI.

CC OS Butithus occitanus tunetanus (Common European scorpion).

CC OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Butithidae; Butithus.

CC RN [1]

CC RP SEQUENCE.

CC RC TISSUE=Venom; MEDLINE=81224814; PubMed=6729843;

CC RA Martin M.-F.; Rochat H.; RT "Purification of thirteen toxins active on mice from the venom of the North African scorpion *Butithus occitanus tunetanus*.";

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 02-FEB-2003 (Rel. 41, Last annotation update)
 DE Toxin SNX-482.
 OS Hysterocrotes gigas (African tarantula).
 OC Karyote; Metaco; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Hysterocrotidae.
 OX NCBI_TaxID=118972;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=99017883; PubMed=9799496;
 RA Newcomb R., Szoke B., Palma A., Wang G., Chen X.-H., Hopkins W.,
 RA Cong R., Miller J., Urge L., Taroczky Hornoch K., Lemos J., Dooley D.J.,
 RA Nadasi L., Tsien R.W., Lemos J., Wilairach G./
 RT "Selective peptide antagonist of the class E calcium channel from the
 RT venom of the tarantula Hysterocrotus gigas.";
 RL Biochemistry 37:15353-15362(1998).
 CC -!- FUNCTION: POTENT AND SELECTIVE BLOCKER OF THE CLASS E CALCIUM
 CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITOR
 CC TOXIN FAMILY.
 DR HSPP; P5652; IDIH.
 DR Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor.
 KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor.
 SQ Sequence 41 AA; 4501 MW; C53CC6D30CFF4 CRC64;

Query Match Score 46; DB 1; Length 41;
 Best Local Similarity 33.3%; Pred. No. 83;
 Matches 11; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

QY 48 GLERKNYCRNPDG--DINGPWCYTMMPRKLFDYC 78
 Db 1 :!| | :!| | :!| | :!| |
 1 GVDAGCRYMFGGCSYNDDOCPRLGCHSLFSYC 33

RESULT 14
 TX51 DENTA STANDARD; PRT; 61 AA.
 ID TX51_DENTA
 AC P01413;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 28-FEB-2003 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Toxin S5CL.
 OS Dendroaspis jamesoni kalmoesae (Eastern Jameson's mamba).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scincidae; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Dendroaspis.
 OX NCBI_TaxID=8019;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79232598; PubMed=465532;
 RT Joubert F.J., Taijaard N.;
 RT "Some properties and the complete primary structures of two reduced
 RT and S-carboxymethylated polypeptides (S5CL and S5C10) from
 RT Dendroaspis jamesoni kalmoesae (Jameson's mamba) venom.";
 RL Biochim. Biophys. Acta 579:228-233 (1979).
 CC -!- FUNCTION: INHIBITS ADP-INDUCED PLATELET AGGREGATION AND INHIBITS
 CC THE BINDING OF PURIFIED PLATELET AGGREGATION RECEPTOR GPIB-IIA
 CC TO IMMOBILIZED FIBRINOGEN (BY SIMILARITY TO MAMBIN).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the snake toxin family.
 DR HSSP; P28375; 1DRS.
 DR InterPro; IPR03511; Snake_toxin.
 DR ProDom; PD000206; Snake_toxin_1.
 DR PROSITE; PS00272; SNAKE_TOXIN; FALSE_NEG.
 KW Blood coagulation; Cell adhesion; Toxin.
 FT DISULFID 3 22 BY SIMILARITY.
 FT DISULFID 16 39 BY SIMILARITY.

FT DISULFID 41 53 BY SIMILARITY.
 FT DISULFID 54 59 BY SIMILARITY.
 SITE 45 47 CELL ATTACHMENT SITE (POTENTIAL).
 SITE 61 AA; 7024 MW; 34B25A6D4SF7EEA CRC64;

Query Match Score 9.1%; DB 1; Length 61;
 Best Local Similarity 53.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 54 CRNPDGDINGPWC 66
 Db 41 CTFPRGDGFPGYC 53

RESULT 15
 YG19_VIBVU STANDARD; PRT; 64 AA.
 ID YG19_VIBVU
 AC 08DC30;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypothetical zinc-binding UPF0243 protein VV11619.
 GN VV11619.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=672;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of Vibrio vulnificus CMP6.;"
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- COFACTOR: Binds 1 zinc ion (By similarity).
 CC -!- SIMILARITY: Belongs to the UPF0243 family.
 CC

This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).

CC DR E016802; AA010038_1; ALT_INIT.
 CC DR HRMAP; MF_00649; -; Zinc; Metal-binding, Complete proteome.
 CC KW HYPOTHETICAL PROTEIN; Zinc; Metal-binding, Complete proteome.
 CC METAL 9 ZINC (BY SIMILARITY).
 CC METAL 12 ZINC (BY SIMILARITY).
 CC METAL 28 ZINC (BY SIMILARITY).
 CC METAL 32 ZINC (BY SIMILARITY).
 CC SQ Sequence 64 AA; 7240 MW; AB0627809FFF9FE CRC64;

Query Match Score 46; DB 1; Length 64;
 Best Local Similarity 27.0%; Pred. No. 1.3e+02;
 Matches 17; Conservative 3; Mismatches 23; Indels 20; Gaps 3;

QY 18 TTVTGTPCQ----EWAQOPHRHSTPIFGTNK-----WAGLEKKNYCRNPDGIN 62
 Db 2 TKITIVKCFQCGTNVVEQSPHR --- PFCSSKKQMDGEADEENAIFGAPDMSDS 56

QY 63 GPW 65
 Db 57 DGW 59

Search completed: September 29, 2003, 08:47:29
 Job time : 24 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: September 29, 2003, 08:44:01 ; Search time 94 Seconds
(without alignments)
236.091 Million cell updates/sec

Title: US-10-088-548-8
Perfect score: 508

Sequence: 1 EQDCMFNGKGRGKATTV.....YTMNPRKLFDFCDIPCLASS 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 105943

Minimum DB seq length: 0

Maximum DB seq length: 86

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL_23;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriapl:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	25.6	75	Q9BGN9	Q9BGN9 bos taurus
2	127.5	25.1	60	Q9UKJ7	Q9UKJ7 homo sapien
3	123	24.2	53	Q9U1Z2	Q9U1Z2 homo sapien
4	56	11.0	67	Q9FOV6	Q9FOV6 azoarcus sp
5	54.5	10.7	65	Q9KEPE1	Q9KEPE1 vibrio chol
6	54	10.6	25	Q9UDP8	Q9UDP8 homo sapien
7	53	10.4	84	Q9W0Y8	Q9W0Y8 drosophila
8	51.5	10.1	71	Q9BMD3	Q9BMD3 caenorhabdi
9	51	10.0	65	Q95T45	Q95T45 chilo iride
10	50	9.8	48	Q8TER4	Q8TER4 saccharomyces
11	49.5	9.7	51	Q8SRV2	Q8SRV2 oryza sativa
12	49.5	9.7	68	Q9FBP2	Q9FBP2 xylolla fas
13	48.5	9.5	61	Q89143	Q89143 virusa virus
14	48.5	9.5	85	Q93BM4	Q93BM4 androtonus
15	48.5	9.5	86	Q8ADD0	Q8ADD0 human immun
16	48	9.4	38	Q8WP57	Q8WP57 lutzomyia l

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	25.6	75	Q9BGN9	Q9BGN9 bos taurus
2	127.5	25.1	60	Q9UKJ7	Q9UKJ7 homo sapien
3	123	24.2	53	Q9U1Z2	Q9U1Z2 homo sapien
4	56	11.0	67	Q9FOV6	Q9FOV6 azoarcus sp
5	54.5	10.7	65	Q9KEPE1	Q9KEPE1 vibrio chol
6	54	10.6	25	Q9UDP8	Q9UDP8 homo sapien
7	53	10.4	84	Q9W0Y8	Q9W0Y8 drosophila
8	51.5	10.1	71	Q9BMD3	Q9BMD3 caenorhabdi
9	51	10.0	65	Q95T45	Q95T45 chilo iride
10	50	9.8	48	Q8TER4	Q8TER4 saccharomyces
11	49.5	9.7	51	Q8SRV2	Q8SRV2 oryza sativa
12	49.5	9.7	68	Q9FBP2	Q9FBP2 xylolla fas
13	48.5	9.5	61	Q89143	Q89143 virusa virus
14	48.5	9.5	85	Q93BM4	Q93BM4 androtonus
15	48.5	9.5	86	Q8ADD0	Q8ADD0 human immun
16	48	9.4	38	Q8WP57	Q8WP57 lutzomyia l

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SPTRMBL_23;* Database: SPTRMBL_23;* Date: 2003-09-29 15:58:54 Version: 5.1.6

SEARCHER: SPTRMBL_23;* SEQUENCER: SPTRMBL_23;* SCORER: SPTRMBL_23;*

RA	Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celinker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Krommiller B., Marshall B., Milligan G.H., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whittlefield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of <i>Drosophila melanogaster</i> genome."; Submitted (MAY-2002) to the EMBL/GenBank/DDJB databases.	ID	055745	PRELIMINARY;	PRT;	65 AA.
RA	DR EMBL; AE03465; AAF47291.3; -.	AC	Q8M4Q3;	PRELIMINARY;	PRT;	48 AA.
RA	DR FLYBase; FBgn000920; NadP60E; -.	DT	01-JUN-1998 (TREMBLrel. 06, Created)			
RA	DR Russio S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whittlefield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of <i>Drosophila melanogaster</i> genome."; Submitted (MAY-2002) to the EMBL/GenBank/DDJB databases.	DT	01-JUN-1998 (TREMBLrel. 06, last sequence update)			
RA	DR	DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
RA	DR Whittlefield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of <i>Drosophila melanogaster</i> genome."; Submitted (MAY-2002) to the EMBL/GenBank/DDJB databases.	DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)			
RA	DR	DE Hypothetical 7.5 kDa Protein				
RA	DR	OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).				
RA	DR	Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.				
RA	DR	NCBI_TaxID=10488;				
RA	SEQUENCE 84 AA; 9648 MW; 8668C9865252B777 CRC64;	RN [1]				
RA	Query Match Score 10.4%; Best Local Similarity 25.4%; Matches 16; Conservative 9; Mismatches 18; Indels 20; Gaps 3; Pred. No. 1.3e+02; Pred. 9.	RP SEQUENCE FROM N.A.				
RA	QY 13 RGKAKTTVTPGCPQE-----AAQPFPHRSTIPTGT-----NEWAGIELEKNC 54	RA Bahar U., Tidona C.A., Darai G.; Virus Genes 0:0-0.1997.				
RA	Db 22 RGRRLSITRGT--SSMCGSTASSTRALLPPPARTATCCPANSPPFRSTCTESMRRLTPST 79	DR AF03741; MAB94456.1; -.				
RA	QY 55 RNP 57	KW Hypothetical protein				
RA	Db 80 RRP 82	SEQUENCE 65 AA; 7526 MW; 1DCD213269477488 CRC64;				
RA	QY 39 FIPGTTNKAGLEKKNYCRNPGDINGPWCY-----TANPRKLFEDYCDIPLC 83	RN [1]				
RA	Do 14 FVTLTNTVTAFFPDGMCLNLDSVGEGYCYFRRVESPTTITKN-----YCDYYC 62	DR AF03741; MAB94456.1; -.				
RA	RESULT 8	RP SEQUENCE FROM N.A.				
RA	OBMQD3 PRELIMINARY; PRT; 71 AA.	Q8M4Q3	OBTGTR4 PRELIMINARY;	PRT;	48 AA.	
RA	AC Q8M4Q3;	AC Q8M4Q3;	OBTGTR4	PRT;	48 AA.	
RA	DT 01-OCT-2002 (TREMBLrel. 22, Created)	DT 01-JUN-2002 (TREMBLrel. 21, Created)				
RA	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
RA	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
RA	DE Hypothetical Protein C18A3.10.	DE Hypothetical 5.2 kDa Protein.				
RA	GN C18A3.10.	GN YER088W-A.				
RA	OS Caenorhabditis elegans.	OS Saccharomyces cerevisiae (Baker's yeast).				
RA	RA Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea; Rhabditida; Feiderinae; Caenorhabditis.	OS Saccharomyces cerevisiae (Baker's yeast).				
RA	OC OC Saccharomyces cerevisiae; Saccharomyces; Saccharomyces.	OC Saccharomyces cerevisiae; Saccharomyces; Saccharomyces.				
RA	OX NCBI_TaxID=6239;	OX NCBI_TaxID=4932;				
RA	RN [1]	RN [1]				
RA	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.				
RA	RC STRAIN=Bristol N2; MEDLINE=99069613; PubMed=9851916;	RC STRAIN=Bristol N2; MEDLINE=21624570; PubMed=11753363;				
RA	RX Waterston R.;	RX Kumar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone P., Miller P., Gerstein M.B., Snyder M.;				
RA	RT "Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology." The <i>C. elegans</i> Sequencing Consortium. Science 282:2012-2018(1998).	RT "An integrated approach for finding overlooked genes in yeast." Nac. Biotechnol. 20:58-63(2002).				
RA	RN [2]	RN DR AF419921; AA179334.1; -.				
RA	RP SEQUENCE FROM N.A.	KW Hypothetical protein.				
RA	RC Hallsworth K.; "The sequence of <i>C. elegans</i> cosmid C18A3"; Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.	SEQUENCE 46 AA; 5208 MW; F7C3B1293C8B0202 CRC64;				
RA	RN [3]	RN [1]				
RA	RP Waterston R.; STRAIN=Bristol N2;	Query Match Score 9.8%; Best Local Similarity 35.7%; Matches 10; conservative 5; Indels 2; Gaps 1;				
RA	RC STRAIN=Bristol N2;	QY 53 YCRNPDG--DINGPWCYTMMPRKLFEDYC 78				
RA	RN DR U2844; AAM81117.1; -.	Do 20 YCHSRDGRKPGEHPWFAGVRQTGECC 47				
RA	DR Wormpp; C18A.10; CB11306.	RESULT 11				
RA	KW Hypothetical Protein.	Q8GRV2 PRELIMINARY;	PRT;	51 AA.		
RA	SEQUENCE 71 AA; 8102 MW; 2C3669D844A93AE3 CRC64;	AC Q8GRV2;				
RA	AC Q8GRV2;	DT 01-MAR-2003 (TREMBLrel. 23, Created)				
RA	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
RA	DE P0438G07.15 protein (B112E07.15 protein).	DE P0438G07.15 OR 112E07.15				
RA	GN Orzya sativa (Japanica cultivar-group).	GN Orzya sativa (Japanica cultivar-group).				
RA	OS Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orizeae; Orzya.	OC Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orizeae; Orzya.				
RA	NCBI_TaxID=39347;	NCBI_TaxID=39347;				
RA	RESULT 9					
RA	Q55745					

Search completed: September 29, 2003, 08:49:13
Search time: 08 seconds